

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 26, 2005, 15:28:42 ; Search time 133.689 Seconds
(without alignments)
659.602 Million cell updates/sec

Title: US-09-545-998B-2
Perfect score: 1301
Sequence: 1 MGAWAWLYGVSMCLVLDLQ.....PEERGEQTEKCHLGRWP 228

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 16Dec04: *
1: Geneseqp1980s: *
2: Geneseqp1990s: *
3: Geneseqp2000s: *
4: Geneseqp2001s: *
5: Geneseqp2002s: *
6: Geneseqp2003as: *
7: Geneseqp2003bs: *
8: Geneseqp2004s: *

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1301	100.0	228	2 AAW37838	Aaw37838 Amino aci
2	1301	100.0	228	2 AAW49016	Aaw49016 Mouse glu
3	1301	100.0	228	6 ADA09440	Ada09440 Murine GI
4	1301	100.0	228	8 ADH43110	Adh43110 Mouse glu
5	1079	82.9	222	2 AAW49018	Aaw49018 Mouse glu
6	1079	82.9	224	2 AAW49017	Aaw49017 Mouse glu
7	735.5	56.5	240	8 ADR46662	Adr46662 Cancer-as
8	735.5	56.5	241	2 AAW37839	Aaw37839 Amino aci
9	735.5	56.5	241	2 AAY06605	Aay06605 Human TNF
10	735.5	56.5	241	3 AAB33431	Aab33431 Human PRO
11	735.5	56.5	241	3 AAY71467	Aay71467 Human PRO
12	735.5	56.5	241	3 AAB27651	Aab27651 Human tum
13	735.5	56.5	241	3 AAY95895	Aay95895 Human PRO
14	735.5	56.5	241	3 AAB24409	Aab24409 Human PRO
15	735.5	56.5	241	4 AAB47054	Aab47054 Human PRO
16	735.5	56.5	241	4 AAB20115	Aab20115 Human imm
17	735.5	56.5	241	4 AAB53090	Aab53090 Human ang
18	735.5	56.5	241	4 AAB47289	Aab47289 PRO3164 po
19	735.5	56.5	241	4 AAB50982	Aab50982 Human PRO
20	735.5	56.5	241	4 AAB50910	Aab50910 Human PRO
21	735.5	56.5	241	5 AAE28161	Aae28161 Human TR1
22	735.5	56.5	241	6 AABU08442	Aabu08442 Amino aci
23	735.5	56.5	241	6 AAO16574	Aao16574 Human tum
24	735.5	56.5	241	6 AAO23091	Aao23091 Human ene
25	735.5	56.5	241	7 ADN39966	Adn39966 Cancer/an

26	735.5	56.5	241	8 ADH43131	Adh43131 Human TNF
27	735.5	56.5	241	8 ADL91869	Adl91869 Human PRO
28	735.5	56.5	241	8 ADO20289	Ado20289 Human PRO
29	735.5	56.5	241	8 ADP55559	Adp55559 Human PRO
30	735.5	56.5	241	8 ADT94287	Adt94287 Human PRO
31	734.5	56.5	235	3 AAY44825	Aay44825 Human mol
32	734.5	56.5	235	6 AAO16576	Aao16576 Human tum
33	734.5	56.5	235	6 AAO23093	Aao23093 Human ene
34	703	54.0	228	2 AAW37840	Aaw37840 Truncated
35	703	54.0	228	6 AAO16577	Aao16577 Human tum
36	703	54.0	228	6 AAO23099	Aao23099 Human ene
37	703	54.0	234	3 AAY95879	Aay95879 Human tum
38	703	54.0	234	3 AAY52158	Aay52158 Tumour ne
39	703	54.0	234	5 AAE28158	Aae28158 Human TR1
40	703	54.0	234	6 ABO08439	Abu08439 Amino aci
41	703	54.0	234	6 AAO16575	Aao16575 Human TR1
42	703	54.0	234	6 ADA09435	Ada09435 Human TR1
43	703	54.0	234	6 AAO23092	Aao23092 Human ene
44	703	54.0	234	8 ADH43105	Adh43105 Human TNF
45	703	54.0	234	8 ADO20305	Ado20305 Human PRO

ALIGNMENTS

RESULT 1

AAW37838
ID AAW37838 standard; protein; 228 AA.

AC AAW37838;

DT 28-JUL-1998 (first entry)

DE Amino acid sequence of the mouse 312C2 T cell protein.

KW Mouse 312C2 T cell protein; thymus cell; spleen cell; T cell;

KW antigen-specific T cell proliferation; cytokine production by T-cell;

KW apoptosis; cancer; haematopoietic cells; lymphoid cell;

KW autoimmune disorders.

XX Mus sp.

OS WO9806842-A1.

XX 19-FEB-1998.

XX 14-AUG-1997; 97WO-US013931.

XX 16-AUG-1996; 96US-00689943.

XX 07-OCT-1996; 96US-0027901P.

XX (SCHE) SCHERING CORP.

XX Gorman DM, Randall TD, Zlotnik A;

XX WPI; 1998-159534/14.

XX N-PSDB; AAV19152.

XX Isolated 312C2 T cell gene - used to develop products for treating, e.g. cancers, auto-immune disorders, transplantation rejection and other T cell disorders.

XX Claim 2; Page 57-58; 71pp; English.

XX This is the amino acid sequence of the mouse 312C2 T cell protein. The 312C2 proteins are expressed in thymus cells and are induced on T cells and spleen cells following activation. Engagement of 312C2 stimulates proliferation of T cell clones, antigen-specific proliferation and cytokine production by T-cells, and potentiates T cell expansion or apoptosis. The products can be used in the treatment of conditions associated with abnormal physiology or development, including abnormal proliferation, e.g. cancerous conditions or degenerative conditions. They can be used in the regulation or development of haematopoietic cells,

XX Mus musculus.
 XX US6509173-B1.
 XX 21-JAN-2003.
 XX 21-OCT-1998; 98US-00176200.
 XX 21-OCT-1997; 97US-0063212P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Ni J, Ruben SM;
 XX WPI; 2003-352290/33.
 XX Novel nucleic acids encoding human tumor necrosis factor receptor-like
 XX proteins TR11, TR11SV1 and TR11SV2, useful for treating blood coagulation
 XX disorders, blood platelet disorders, stroke and myocardial infarction.
 XX Disclosure; Fig 4; 70pp; English.
 XX The present invention relates to the isolation of novel human tumor
 XX necrosis factor (TNF) receptor-like proteins, designated TR11, TR11SV1
 XX and TR11SV2 receptors, and the polynucleotide sequences encoding them.
 XX the polypeptide and polynucleotide sequences for TR11, TR11SV1, and
 XX TR11SV2 are useful in assays to test one or more biological activities of
 XX TR11, TR11SV1 and TR11SV2 polypeptides, for proliferation,
 XX differentiation and mobilisation of immune cells, and as markers or
 XX detectors of a particular immune system disease or disorder. They are
 XX also useful in treating or detecting deficiencies or disorders of
 XX haematopoietic cells, to increase differentiation and proliferation of
 XX haematopoietic cells, including pluripotent stem cells in an effort to
 XX treat disorders associated with a decrease in haematopoietic cells e.g.
 XX blood protein disorders, HIV-infection, anaemia and thrombocytopaenia.
 XX The sequences are also useful for modulating haemostatic or thrombolytic
 XX activity, for treating blood coagulation disorders, blood platelet
 XX disorders or wounds resulting from trauma, as well as for treating
 XX stroke, myocardial infarction and scarring. They may be used for
 XX detecting or treating autoimmune disorders (e.g. Addison's disease,
 XX rheumatoid arthritis, dermatitis, allergic encephalomyelitis,
 XX glomerulonephritis, Grave's disease, diabetes mellitus, multiple
 XX sclerosis and autoimmune thyroiditis), for treating allergic reactions
 XX such as asthma, for treating and/or preventing organ rejection or graft
 XX versus host disease (GVHD), for treating hyperproliferative disorders
 XX including neoplasms and cancers, for treating or modulating inflammation
 XX or inflammatory conditions such as inflammation associated with infection
 XX (e.g. septic shock and sepsis, ischaemia-reperfusion injury, endotoxin
 XX lethality, induced lung injury and Crohn's disease), for treating or
 XX detecting infectious agents such as viruses, bacteria, parasites and
 XX fungi, for differentiating, proliferating and attracting cells for tissue
 XX regeneration, and as vaccines to raise immune response against infectious
 XX diseases. The polynucleotide sequences are also useful in ex vivo gene
 XX therapy, and for proliferating and differentiating peripheral nervous
 XX system diseases such as spinal cord disorders, cerebrovascular diseases,
 XX Alzheimer's disease, Parkinson's disease, Huntington's disease,
 XX amyotrophic lateral sclerosis and Shy-Drager syndrome. The present
 XX sequence represents murine glucocorticoid-induced tumour necrosis factor
 XX receptor family related protein (GTR).
 XX Sequence 228 AA;
 XX Query Match 100.0%; Score 1301; DB 6; Length 228;
 XX Best Local Similarity 100.0%; Pred. No. 1.6e-112;
 XX Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGAWMLYGVSMLCVLDLGGPSVVEPCGPGKVGSGNNTCCSLYAPKEDCPKRC 60
 Db 1 MGAWMLYGVSMLCVLDLGGPSVVEPCGPGKVGSGNNTCCSLYAPKEDCPKRC 60
 QY 61 ICVTPEVHCSDPCKICKYPCQGRVESQGDIVFGFRVCACAMGTFSAGRDGHCR LWT 120

Db 61 ICVTPEVHCSDPCKICKYPCQGRVESQGDIVFGFRVCACAMGTFSAGRDGHCR LWT 120
 QY 121 NCSQFGFLTFPGNKTNAVCIPEPLPTEQYGH LTVIELVMAACIFFLTTVQLGHLH IWL 180
 Db 121 NCSQFGFLTFPGNKTNAVCIPEPLPTEQYGH LTVIELVMAACIFFLTTVQLGHLH IWL 180
 QY 181 RRQHMCPRETQPPFAEVQLSADACSFPQPEBERGEQTEKCHLGGRWP 228
 Db 181 RRQHMCPRETQPPFAEVQLSADACSFPQPEBERGEQTEKCHLGGRWP 228
 RESULT 4
 ADH43110
 ID ADH43110 standard; protein; 228 AA.
 XX
 AC ADH43110;
 XX
 DT 25-MAR-2004 (first entry)
 XX
 DE Mouse glucocorticoid-induced tumour necrosis factor receptor (GTR).
 XX
 KW antiinflammatory; osteopathic; immunosuppressive; neuroprotective;
 KW immunostimulant; antirheumatic; dermatological; antithyroid; haemostatic;
 KW antischismatic; antiarthritic; cytostatic; proliferation inhibitor;
 KW differentiation inhibitor; T-cell chemotaxis inhibitor;
 KW B-cell chemotaxis inhibitor; haemostasis; thrombolytic activity;
 KW TR11SV1; TR11SV2; tumour necrosis factor receptor-like protein;
 KW TNF receptor-like protein; inflammation; bone disease; Paget's disease;
 KW osteoporosis; craniofacial dysplasia;
 KW fibrodysplasia ossificans progressiva; gigantism; osteoclastoma;
 KW autoimmune disorder; autoimmune haemolytic anaemia; autoimmunocytopenia;
 KW multiple sclerosis; autoimmune thyroiditis; immunodeficiency disorder;
 KW severe combined immunodeficiency; Wiskott-Aldrich syndrome;
 KW rheumatoid arthritis; systemic lupus erythematosus;
 KW graft-versus-host disease; asthma; cancer; Grave's disease;
 KW blood coagulation disorder; platelet disorder; thrombocytopenia; TR11;
 KW tumour necrosis factor receptor family; mouse;
 KW glucocorticoid-induced tumour necrosis factor receptor; GTR.
 XX
 OS Mus musculus.
 XX
 PN US2003138426-A1.
 XX
 PD 24-JUL-2003.
 XX
 XX 30-OCT-2002; 2002US-00283105.
 XX
 XX 21-OCT-1997; 97US-0063212P.
 XX 21-OCT-1998; 98US-00176200.
 XX 24-FEB-1999; 99US-0121648P.
 XX 13-MAY-1999; 99US-0134172P.
 XX 16-JUL-1999; 99US-0144076P.
 XX 23-FEB-2000; 2000US-00512363.
 XX 28-JUL-2000; 2000US-0221577P.
 XX 27-JUL-2001; 2001US-00915593.
 XX 30-OCT-2001; 2001US-0330757P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Ni J, Ruben SM;
 XX WPI; 2004-068938/07.
 XX
 XX Novel isolated antibody binding to TR11SV1/TR11SV2 receptor, useful for
 XX treating inflammation, Paget's disease, thyroiditis.
 XX Disclosure; SEQ ID NO 7; 135pp; English.
 XX The invention describes an isolated antibody (I) or its portion
 XX specifically binding to a protein chosen from a protein with amino acid
 XX residues 1-62 or 51-62 of a fully defined TR11SV1 receptor sequence of
 XX 241 amino acids (S1) as given in specification, and a protein with amino
 XX acid residues 38-49 of a fully defined TR11SV2 receptor sequence of 240

CC amino acids as given in specification. (I) is useful for detecting tumour
 CC necrosis factor (TNF) receptor-like proteins TRILSV1 or TRILSV2 protein
 CC in a biological sample, which involves contacting the biological sample
 CC with (I), and detecting the TRILSV1 or TRILSV2 protein in the biological
 CC sample. (I) is a labeled antibody, the label is chosen from an enzyme
 CC label, a radioisotope, a fluorescent label, and biotin. The method
 CC described is useful for treating inflammation. Also described is a method
 CC useful for treating bone disease or a disorder such as Paget's disease,
 CC osteoporosis, craniometaphyseal dysplasia, fibrodysplasia ossificans
 CC progressiva, gigantism, or osteoclastoma. (I) is useful for treating
 CC autoimmune disorders e.g. autoimmune haemolytic anaemia,
 CC immunodeficiency disorders e.g. severe combined immunodeficiency, etc.,
 CC autoimmune thyroiditis, multiple sclerosis, autoimmune thyroiditis, etc.,
 CC Wiskott-Aldrich syndrome. (I) is also useful for treating rheumatoid
 CC arthritis, systemic lupus erythematosus, graft-versus-host disease,
 CC asthma, cancer, Grave's disease, blood coagulation disorders and platelet
 CC disorders (thrombocytopenia). This is the amino acid sequence of mouse
 CC glucocorticoid-induced tumour necrosis factor receptor (Gitr) used in a
 CC comparison with the novel tumour necrosis factor receptor family members
 CC TRIL1, TRILSV1 and TRILSV2.
 XX
 SQ Sequence 228 AA;

Query Match 100.0%; Score 1301; DB 8; Length 228;
 Best Local Similarity 100.0%; Pred. No. 1.6e-112; Mismatches 0; Gaps 0;
 Matches 228; Conservative 0; Indels 0; Gaps 0;
 QY 1 MGAWMLYGVSMCLVDLQGPSVVEEPCGPGKVGSGNNTRCCSLYAPGKEDCPKERC 60
 DB 1 MGAWMLYGVSMCLVDLQGPSVVEEPCGPGKVGSGNNTRCCSLYAPGKEDCPKERC 60
 QY 61 ICVTPEYHCGDPQCKICKHYPCQPQORVESQGDIVFGFRCVACAMGTFSAGRDGHCRLWT 120
 DB 61 ICVTPEYHCGDPQCKICKHYPCQPQORVESQGDIVFGFRCVACAMGTFSAGRDGHCRLWT 120
 QY 121 NCSQFGFLTMFPGNKNTHNAVCIPEPLPTEQYGHLLTVIFLVMAACIFFLTTVOLGLHIWOL 180
 DB 121 NCSQFGFLTMFPGNKNTHNAVCIPEPLPTEQYGHLLTVIFLVMAACIFFLTTVOLGLHIWOL 180
 QY 181 RQHMCPRETQPPFAEVLQSAEDACSFQFPEERGERQTEKCHLGGWRP 228
 DB 181 RQHMCPRETQPPFAEVLQSAEDACSFQFPEERGERQTEKCHLGGWRP 228

RESULT 5
 AAW49018
 ID AAW49018 standard; protein; 222 AA.
 AC AAW49018;
 XX
 XX 29-SEP-1998 (first entry)
 DE Mouse glucocorticoid induced TNFR-family related protein variant C.
 XX
 KW Mouse glucocorticoid induced TNFR-family related protein; lymphocyte;
 KW Gitr; tumour necrosis factor; apoptosis; hodgkin's disease; Gitr-B;
 KW Gitr-C.
 XX
 OS Mus sp.
 XX
 PN WO9824895-A1.
 XX
 PD 11-JUN-1998.
 XX
 PF 08-NOV-1997; 97WO-EP006252.
 XX
 PR 02-DEC-1996; 96GB-00025074.
 XX
 XX (PHAA) PHARMACIA & UPJOHN SPA.
 PA
 PI Riccardi C;
 XX
 DR WPI; 1998-333315/29.
 XX
 XX
 PT New isolated glucocorticoid induced TNFR related polypeptide - used to

DR N-PSDB; AAV32775.
 XX
 PT New isolated glucocorticoid induced TNFR related polypeptide - used to
 PT stimulate lymphocyte activity and cell death rescue, useful to, e.g.
 PT develop products to suppress lymphocyte activity and induce apoptosis.
 XX
 PS Claim 15; Page 43-44; 53pp; English.
 XX
 CC The present claimed sequence represents a mouse glucocorticoid induced
 CC TNFR-family related protein variant C (Gitr-C). The invention also claims
 CC for Gitr (AAW49016) and Gitr-B (AAW49017). The Gitr's are claimed to be
 CC useful for stimulating lymphocyte activity and cell death rescue. Gitr
 CC antagonists are claimed to be useful for suppressing the lymphocyte
 CC activity and for inducing apoptotic deletion. Gitr cDNAs and the proteins
 CC they encode are also claimed to be useful for suppressing growth of
 CC tumour cells over-expressing Gitr or for the treatment of refractory
 CC hodgkin's disease
 XX
 SQ Sequence 222 AA;

Query Match 82.9%; Score 1079; DB 2; Length 222;
 Best Local Similarity 100.0%; Pred. No. 6.4e-92;
 Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGAWMLYGVSMCLVDLQGPSVVEEPCGPGKVGSGNNTRCCSLYAPGKEDCPKERC 60
 DB 1 MGAWMLYGVSMCLVDLQGPSVVEEPCGPGKVGSGNNTRCCSLYAPGKEDCPKERC 60
 QY 61 ICVTPEYHCGDPQCKICKHYPCQPQORVESQGDIVFGFRCVACAMGTFSAGRDGHCRLWT 120
 DB 61 ICVTPEYHCGDPQCKICKHYPCQPQORVESQGDIVFGFRCVACAMGTFSAGRDGHCRLWT 120
 QY 121 NCSQFGFLTMFPGNKNTHNAVCIPEPLPTEQYGHLLTVIFLVMAACIFFLTTVOLGLHIWOL 180
 DB 121 NCSQFGFLTMFPGNKNTHNAVCIPEPLPTEQYGHLLTVIFLVMAACIFFLTTVOLGLHIWOL 180
 QY 181 RQHMCPR 188
 DB 181 RQHMCPR 188

RESULT 6
 AAW49017
 ID AAW49017 standard; protein; 294 AA.
 AC AAW49017;
 XX
 XX 29-SEP-1998 (first entry)
 DE Mouse glucocorticoid induced TNFR-family related protein variant B.
 XX
 KW Mouse glucocorticoid induced TNFR-family related protein; lymphocyte;
 KW Gitr; tumour necrosis factor; apoptosis; hodgkin's disease; Gitr-B;
 KW Gitr-C.
 XX
 OS Mus sp.
 XX
 PN WO9824895-A1.
 XX
 PD 11-JUN-1998.
 XX
 PF 08-NOV-1997; 97WO-EP006252.
 XX
 PR 02-DEC-1996; 96GB-00025074.
 XX
 XX (PHAA) PHARMACIA & UPJOHN SPA.
 PA
 PI Riccardi C;
 XX
 DR WPI; 1998-333315/29.
 XX
 XX N-PSDB; AAV32774.
 XX
 PT New isolated glucocorticoid induced TNFR related polypeptide - used to

PT stimulate lymphocyte activity and cell death rescue, useful to, e.g.
 PI develop products to suppress lymphocyte activity and induce apoptosis.
 XX Claim 14; Page 40-41; 53pp; English.
 XX The present claimed sequence represents a mouse glucocorticoid induced
 CC TNFR-family related protein variant B (GTR-B). The invention also claims
 CC for GTR (AAW49016) and GTR-C (AAW49018). The GTRs are claimed to be
 CC useful for stimulating lymphocyte activity and cell death rescue. GTR
 CC antagonists are claimed to be useful for suppressing the lymphocyte
 CC activity and for inducing apoptotic deletion. GTR cDNAs and the proteins
 CC they encode are also claimed to be useful for suppressing growth of
 CC tumour cells over-expressing GTR or for the treatment of refractory
 CC hodgkin's disease
 XX Sequence 294 AA;
 SQ
 Query Match 82.9%; Score 1079; DB 2; Length 294;
 Best Local Similarity 100.0%; Pred. No. 8.9e-92;
 Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGAWMLYGVSMCLVDLQPSVVEPGCGPKGVQNGSGNTRCCSLYAPGKEDCPKERC 60
 DB 1 MGAWMLYGVSMCLVDLQPSVVEPGCGPKGVQNGSGNTRCCSLYAPGKEDCPKERC 60
 QY 61 ICVTPEYHCGDPQCKICKHYPCQPGORVESQGDIVFGPRCVACAMGTFPSAGRDGHCRLWT 120
 DB 61 ICVTPEYHCGDPQCKICKHYPCQPGORVESQGDIVFGPRCVACAMGTFPSAGRDGHCRLWT 120
 QY 121 NCSQGFGLTFMFGNKTNAVCIPPELPTQYGHILTIVIFLVMAACIFFLTTVOLGLHIWOL 180
 DB 121 NCSQGFGLTFMFGNKTNAVCIPPELPTQYGHILTIVIFLVMAACIFFLTTVOLGLHIWOL 180
 QY 181 RQHMCPR 188
 DB 181 RQHMCPR 188
 RESULT 7
 ADR46662
 ID ADR46662 standard; protein; 240 AA.
 AC ADR46662;
 XX 18-NOV-2004 (first entry)
 DT Cancer-associated protein, SEQ ID 75.
 DE Cytostatic; Gene Therapy; cancer; human.
 KW Cytostatic; Gene Therapy; cancer; human.
 XX Homo sapiens.
 OS WO2004073657-A2.
 XX WO2004073657-A2.
 PN 02-SEP-2004.
 PD 19-FEB-2004; 2004WO-US005455.
 PF 19-FEB-2003; 2003US-0448784P.
 XX (PROT-) PROTEIN DESIGN LABS INC.
 PA Aziz N, Gish KC, Wilson KE, Zlotnik A;
 PI WPI; 2004-652787/63.
 XX N-PSDB; ADR46604.
 DR Detecting a pathological cell in a patient for diagnosing or treating
 PT cancer by detecting in a biological sample from the patient genes whose
 PT expression are up-regulated or down-regulated in specific cancers.
 XX Claim 1; SEQ ID NO 75; 375pp; English.

CC The present invention relates to a method for detecting cancer in a
 CC patient. The method comprises detecting in a biological sample from the
 CC patient a nucleotide or protein sequence comprising a sequence that is at
 CC least 80% identical to a nucleotide sequence (ADR46588-ADR46645) or
 CC protein sequence (ADR46646-ADR46703). The method is useful for detecting
 CC cancer for preparing a composition for diagnosing or treating cancer.
 XX Sequence 240 AA;
 SQ
 Query Match 56.5%; Score 735.5; DB 8; Length 240;
 Best Local Similarity 57.0%; Pred. No. 5.7e-60;
 Matches 134; Conservative 31; Mismatches 61; Indels 9; Gaps 3;
 QY 1 MGAWMLYGVSMCLVDLQPSVVEPGCGPKGVQNGSGNTRCCSLYA-----PGKE 53
 DB 7 MGAPRALCGLALLCALSLGQ-RPTGGPGCGPGRLLLTGTDAACRVHTTCCRDYPGEE 65
 QY 54 DCPKERCICVTPEYHCGDPQCKICKHYPCQPGORVESQGDIVFGPRCVACAMGTFPSAGRD 113
 DB 66 CGSEWDNCVQPEFHCPCCTTCRHHPCPPGQGVQSQKFSFGQCIDCAGTSGGHE 125
 QY 114 GHCLRWNTCSQGFGLTFMFGNKTNAVCIPPELPTQYGHILTIVIFLVMAACIFFLTTVOL 173
 DB 126 GHCKPWTCTQGFGLTFMFGNKTNAVCIPPELPTQYGHILTIVIFLVMAACIFFLTTVOL 185
 QY 174 GLHIWQLRRQHCMPRETQPFAPVQLSADACSFQPFPEERGSQT-EEKCHLGRW 227
 DB 186 GLHIWQLRSQCMWPRETQLLLEVPSTEDARSCQPFPEERGSABEKGRLGLDW 240
 RESULT 8
 AAW37839
 ID AAW37839 standard; protein; 241 AA.
 XX AAW37839;
 AC AAW37839;
 XX 28-JUL-1998 (first entry)
 DT Amino acid sequence of the human 312C2 T cell protein.
 DE Human 312C2 T cell protein; thymus cell; spleen cell; T cell;
 KW antigen-specific T cell proliferation; cytokine production by T-cell;
 KW apoptosis; cancer; haematopoietic cells; lymphoid cell;
 KW autoimmune disorders.
 XX Homo sapiens.
 OS WO9806842-A1.
 XX WO9806842-A1.
 PN 19-FEB-1998.
 PD 14-AUG-1997; 97WO-US013931.
 PF 16-AUG-1996; 96US-00689943.
 XX 07-OCT-1996; 96US-0027901P.
 PR (SCHE) SCHERING CORP.
 PA Gorman DM, Randall TD, Zlotnik A;
 XX WPI; 1998-159534/14.
 DR N-PSDB; AAV19153.
 XX Isolated 312C2 T cell gene - used to develop products for treating, e.g.
 PT cancers, auto-immune disorders, transplantation rejection and other T
 PT cell disorders.
 XX Claim 2; Page 59-60; 71pp; English.
 PS This is the amino acid sequence encoding the human 312C2 T cell protein.
 XX The 312C2 proteins are expressed in thymus cells and are induced on T
 CC cells and spleen cells following activation. Engagement of 312C2
 CC stimulates proliferation of T cell clones, antigen-specific proliferation

CC and cytokine production by T-cells, and potentiates T cell expansion or
 CC apoptosis. The products can be used in the treatment of conditions
 CC associated with abnormal physiology or development, including abnormal
 CC proliferation, e.g. cancerous conditions or degenerative conditions. They
 CC can be used in the regulation or development of haematopoietic cells,
 CC e.g. lymphoid cells which affect immunological responses, e.g. autoimmune
 CC disorders

SQ Sequence 241 AA;
 Query Match 56.5%; Score 735.5; DB 2; Length 241;
 Best Local Similarity 57.0%; Pred. No. 5.8e-60;
 Matches 134; Conservative 31; Mismatches 61; Indels 9; Gaps 3;
 QY 1 MGAWAMLYGVSMCLVLDLGPQSVVEEPCGCGKVGQSGNNTRCCSLYA-----PGKE 53
 DB 7 MGAFAALCGLALLCALSLGQ-RPTGGPGCGPRLLLGTGTARCCRVHTTRCCRDYPGEE 65
 QY 54 DCPKERCICVTPEYHCGDPQCKICKHYPCQPCQVQSGQDIVFGPCVACAMGTFSAGRD 113
 DB 66 CCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSGKFSFGQCDICASGTFSGGHE 125
 QY 114 GHCLRWNTCSQFGFLTPFPNGKTHNAVCIPEPLPTEQYGHLLTVIFLVMAACIFFLTITVQL 173
 DB 126 GHCKPWTDTCTQFGFLTVFPNGKTHNAVCPGSPPAEPLGLWLTVLLVAACVLLLTSAQL 185
 QY 174 GLHIWQLRQHCMPRETQFAEVQLSAEDACSFQPPPEERGBOT-EEKCHLGGRW 227
 DB 186 GLHIWQLRSQCMWPRETQLLEVPSTEDARSCQFPPEERGBERSAEKRGDLW 240

RESULT 9
 AAY06605
 ID AAY06605 standard; protein; 241 AA.
 AC AAY06605;
 XX
 DT 26-OCT-1999 (first entry)
 DE Human TNF receptor homologue PRO364.
 KW PRO364; tumour necrosis factor receptor; human; apoptosis; inflammation;
 KW antiinflammatory; NF-KB activation; autoimmune disease; therapy.
 XX
 OS Homo sapiens.

Key	Location/Qualifiers
FT Peptide	1..25 "signal peptide"
FT Protein	26..241
FT Modified-site	146 "mature protein"
FT Domain	162..180 "N-glycosylated"
FT	/note= "transmembrane domain"
XX	
PN	WO9940196-A1.
XX	
PD	12-AUG-1999.
XX	
PF	09-FEB-1999; 99WO-US002642.
XX	
PR	09-FEB-1998; 98US-0074087P.
XX	
PA	(GETH) GENENTECH INC.
XX	
PI	Ashkenazi AJ, Gurney AL, Marsters SA, Pitti RM, Wood WI;
PI	Goddard A;
XX	
DR	WPI; 1999-494296/41.
DR	N-PSDB; AAX87670.
XX	
PT	Tumor necrosis factor receptor homologue - useful for, e.g. modulating

PT apoptosis and NF-KB activation and proinflammatory or autoimmune
 PT responses.
 XX Claim 17; Fig 2A; 104pp; English.
 XX
 CC The present sequence represents human PRO364, a novel member of the
 CC tumour necrosis factor receptor family. The sequence was deduced from a
 CC bone marrow cDNA clone (see AAX87670). Methods for the recombinant
 CC production of PRO364 polypeptides, e.g. in CHO, Escherichia coli or yeast
 CC host cells, are provided. Claimed polypeptides comprise amino acids 1-
 CC 241, 1-X, 26-241 (i.e. the mature protein) and 26-X of the present
 CC sequence, where X is any one of amino acid residues 157-167 of PRO364.
 CC PRO364 polypeptides are useful for modulating apoptosis, NF-KB activation
 CC and proinflammatory or autoimmune responses in mammalian cells (claimed).
 CC Chimeric molecules comprising a PRO364 polypeptide fused to a
 CC heterologous sequence such as epitope tag or immunoglobulin Fc region are
 CC also claimed. PRO364 can be used in assays to identify other proteins or
 CC molecules involved in binding interactions. This is useful for
 CC identifying inhibitors or agonists of receptor/ligand binding. The PRO364
 CC polypeptides may also be combined with an agent that is cytotoxic,
 CC chemotherapeutic or a growth inhibitor. PRO364 antibodies are useful in
 CC diagnostic methods, purification methods and also in therapy, e.g. as
 CC inhibitors

SQ Sequence 241 AA;
 Query Match 56.5%; Score 735.5; DB 2; Length 241;
 Best Local Similarity 57.0%; Pred. No. 5.8e-60;
 Matches 134; Conservative 31; Mismatches 61; Indels 9; Gaps 3;
 QY 1 MGAWAMLYGVSMCLVLDLGPQSVVEEPCGCGKVGQSGNNTRCCSLYA-----PGKE 53
 DB 7 MGAFAALCGLALLCALSLGQ-RPTGGPGCGPRLLLGTGTARCCRVHTTRCCRDYPGEE 65
 QY 54 DCPKERCICVTPEYHCGDPQCKICKHYPCQPCQVQSGQDIVFGPCVACAMGTFSAGRD 113
 DB 66 CCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSGKFSFGQCDICASGTFSGGHE 125
 QY 114 GHCLRWNTCSQFGFLTPFPNGKTHNAVCIPEPLPTEQYGHLLTVIFLVMAACIFFLTITVQL 173
 DB 126 GHCKPWTDTCTQFGFLTVFPNGKTHNAVCPGSPPAEPLGLWLTVLLVAACVLLLTSAQL 185
 QY 174 GLHIWQLRQHCMPRETQFAEVQLSAEDACSFQPPPEERGBOT-EEKCHLGGRW 227
 DB 186 GLHIWQLRSQCMWPRETQLLEVPSTEDARSCQFPPEERGBERSAEKRGDLW 240

RESULT 10
 AAB33431
 ID AAB33431 standard; protein; 241 AA.
 XX
 AC AAB33431;
 XX
 DT 29-JAN-2001 (first entry)
 XX
 DE Human PRO364 protein UNQ319 SEQ ID NO:92.

XX	Human; immune related disease; diagnosis; antiinflammatory; cardiant;
KW	dermatological; antiarthritic; antirheumatic; immunosuppressive;
KW	haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;
KW	antianemic; hepatotropic; virucide; antipsoriatic; antiallergic;
KW	antiaschmatic; systemic lupus erythematosus; rheumatoid arthritis;
KW	osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;
KW	idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
KW	systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
KW	autoimmune thrombocytopaenia; immune-mediated renal disease;
KW	demyelinating disease; hepatobiliary disease; Whipple's disease;
KW	inflammatory bowel disease; gluten-sensitive enteropathy;
KW	autoimmune disease; immune-mediated skin disease; allergic disease;
KW	immunological disease; transplantation associated disease;
KW	graft rejection; graft-versus-host-disease.
XX	
OS	Homo sapiens.

XX	WO200053758-A2.	CC	disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune
PN		CC	or immune-mediated skin diseases, allergic diseases, immunological
PD		CC	diseases of the lung, and transplant-associated diseases including
PI	14-SEP-2000.	CC	graft rejection and graft-versus-host-disease. AAC58397 to AAC58578
PF		CC	represent PCR primers and hybridisation probes used in the isolation of
PG		CC	human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB33477
PH		CC	represent human PRO polynucleotide and protein sequences given in the
PI	02-MAR-2000; 2000WO-US005841.	CC	exemplification of the present invention
PP		XX	Sequence 241 AA;
PR	08-MAR-1999; 99WO-US005028.	SQ	
PR	10-MAR-1999; 99US-0123618P.		
PR	12-MAR-1999; 99US-0123957P.		
PR	23-MAR-1999; 99US-0125775P.		
PR	12-APR-1999; 99WO-US028849P.		
PR	20-APR-1999; 99WO-US008615.		
PR	28-APR-1999; 99US-0131445P.		
PR	04-MAY-1999; 99US-0132371P.		
PR	14-MAY-1999; 99US-0134287P.		
PR	02-JUN-1999; 99WO-US012252.		
PR	23-JUN-1999; 99US-0141037P.		
PR	20-JUL-1999; 99US-0144758P.		
PR	26-JUL-1999; 99US-0145698P.		
PR	28-JUL-1999; 99US-0146222P.		
PR	01-SEP-1999; 99WO-US020111.		
PR	08-SEP-1999; 99WO-US020594.		
PR	13-SEP-1999; 99WO-US020944.		
PR	15-SEP-1999; 99WO-US021090.		
PR	15-SEP-1999; 99WO-US021547.		
PR	05-OCT-1999; 99WO-US023089.		
PR	29-OCT-1999; 99US-0162506P.		
PR	29-NOV-1999; 99WO-US028214.		
PR	30-NOV-1999; 99WO-US028313.		
PR	30-NOV-1999; 99WO-US028409.		
PR	01-DEC-1999; 99WO-US028301.		
PR	01-DEC-1999; 99WO-US028634.		
PR	02-DEC-1999; 99WO-US028551.		
PR	02-DEC-1999; 99WO-US028564.		
PR	02-DEC-1999; 99WO-US028565.		
PR	16-DEC-1999; 99WO-US030095.		
PR	20-DEC-1999; 99WO-US030999.		
PR	30-DEC-1999; 99WO-US031274.		
PR	05-JAN-2000; 2000WO-US000219.		
PR	06-JAN-2000; 2000WO-US000277.		
PR	11-FEB-2000; 2000WO-US000376.		
PR	18-FEB-2000; 2000WO-US003565.		
PR	18-FEB-2000; 2000WO-US004341.		
PR	22-FEB-2000; 2000WO-US004342.		
XX	22-FEB-2000; 2000WO-US004414.		
PA	(GETH) GENENTECH INC.		
XX			
PI	Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;		
PI	Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;		
PI	Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;		
XX			
DR	WPI: 2000-572271/53.		
DR	N-PSDB; AAC58596.		
XX			
PT	Sixty four PRO polypeptides, useful in the diagnosis and treatment of		
PT	immune related disorders, e.g. systemic lupus erythematosus, rheumatoid		
PT	arthritis, osteoarthritis, thyroiditis and diabetes mellitus.		
XX			
XX	Claim 33; Fig 36; 309pp; English.		
XX			
CC	The present invention describes sixty four human PRO proteins which can		
CC	be used in the treatment of immune related diseases. The human PRO		
CC	proteins, anti-PRO antibodies, agonists and antagonists are useful for		
CC	treating and diagnosing immune related disorders. The disorders are		
CC	selected from systemic lupus erythematosus, rheumatoid arthritis,		
CC	osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,		
CC	systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's		
CC	syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic		
CC	anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,		
CC	immune-mediated renal disease, demyelinating diseases of the central and		
CC	peripheral nervous systems, hepatobiliary diseases, inflammatory bowel		

CC	disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune
CC	or immune-mediated skin diseases, allergic diseases, immunological
CC	diseases of the lung, and transplantation associated diseases including
CC	graft rejection and graft-versus-host-disease. AAC58397 to AAC58578
CC	represent PCR primers and hybridisation probes used in the isolation of
CC	human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB33477
CC	represent human PRO polynucleotide and protein sequences given in the
CC	exemplification of the present invention
XX	
XX	Sequence 241 AA;
QY	Query Match 56.5%; Score 735.5; DB 3; Length 241;
DB	Best Local Similarity 57.0%; Pred. No. 5.8e-60;
DB	Matches 134; Conservative 31; Mismatches 61; Indels 9; Gaps 3;
QY	1 MGAWAMLYGVSMLCVLDLQPSVVEPGCGKVGQNGSNTRCCSLYA-----PQKE 53
DB	7 MGAFAALCGLALLCALSLQG-RPTGGPGCGGPRLLLTGTGDARCCRVHTTRCCRDYPGEE 65
QY	54 DCPKERCICVTPPYHCGDDPOCKICKHYPCQPGQRVESQGLIVGRCVACAMGTFSAGRD 113
DB	66 CCSEWDCMCVQPEFHCGDPCCCTTCHHPCPPGQGVQSGKFSFGFCIDCASGTFSGGHE 125
QY	114 GHCLWNTCSQFGFLTMPFGNKNTHNAVCIPEPLPTEQYGHLYVIFLVMAACIFELTTVOL 173
DB	126 GHCKPMTDCTQFGFLTFVPGNKNTHNAVCPGSPPAEPLGLWLTVLLVAACVLLLTSAQL 185
QY	174 GLHIWLRQHCMPRETQPPFAEVQLSAEDACSFQPEEREGEQT-EKCHLGGRW 227
DB	186 GLHIWLRQSCMPRETQLLLEVPSTEDARSCQPEERGERSAEKGRGLDLW 240
RESULT 11	
AA71467	
ID	AA71467 standard; protein; 241 AA.
XX	
AC	AA71467;
XX	
DT	08-NOV-2000 (first entry)
XX	
DE	Human PRO364 protein.
XX	
KW	PRO364; DNA47365-1206; human; ATCC No: 209436; antiproliferative;
KW	neoplastic cell growth inhibitor; cytostatic; treatment; cancer; tumour;
KW	breast; prostate; colon; lung; renal; ovarian; central nervous system;
KW	CNS; leukemia; melanoma; Expressed Sequence Tag; EST; TNFR homologue;
KW	tumour necrosis factor receptor; GTR protein homologue.
XX	
OS	Homo sapiens.
XX	
PH	Key Location/Qualifiers
FT	Peptide 1..25
FT	Modified-site /label= Signal_peptide
FT	Modified-site /note= "N-myristoylation site"
FT	Modified-site 8..14
FT	Modified-site /note= "N-myristoylation site"
FT	Modified-site 25..31
FT	Modified-site /note= "N-myristoylation site"
FT	Protein 26..241
FT	Modified-site /label= Mature_PRO364_protein
FT	Modified-site 30..36
FT	Modified-site /note= "N-myristoylation site"
FT	Modified-site 33..39
FT	Modified-site /note= "N-myristoylation site"
FT	Modified-site 118..124
FT	Modified-site /note= "N-myristoylation site"
FT	Modified-site 122..128
FT	Modified-site /note= "N-myristoylation site"
FT	Modified-site 146..150
FT	Modified-site /note= "Asn is N-glycosylated"
FT	Modified-site 156..162
FT	Modified-site /note= "N-myristoylation site"

```

FT Domain 163..183
FT /label= Transmembrane_domain
FT Binding-site 166..177
FT /note= "Prokaryotic membrane lipoprotein lipid attachment
FT site"
FT Region 171..193
FT /note= "Leucine zipper pattern"
XX WO200032778-A2.
XX 08-JUN-2000.
XX
XX 30-NOV-1999; 99WO-US028409.
XX
XX 01-DEC-1998; 98WO-US025108.
XX 16-DEC-1998; 98US-01128508.
XX 22-DEC-1998; 98US-01132968.
XX 20-JUL-1999; 99US-0144758P.
XX 26-JUL-1999; 99US-0145698P.
XX
XX (GETH ) GENENTECH INC.
XX
XX Chen J, Goddard A, Gurney AL, Hillan K, Napier M, Wood WI;
XX WPI; 2000-412325/35.
XX N-PSDB; AAD01240.
XX
XX New composition useful for inhibiting neoplastic cell growth and for
XX treating cancers, comprises PRO655, PRO344 or PRO364 polypeptide or their
XX antagonists.
XX
XX Claim 31; Fig 4; 108pp; English.
XX
XX The present sequence is the human PRO364 protein, encoded by the cDNA
XX clone, designated as DNA47365-1206. It is isolated from human small
XX intestine tissue cDNA library, identified using probes based on the
XX consensus sequence DNA44825, relative to the Incyte expressed sequence
XX tag (EST) 3003460. This EST has homology to tumour necrosis factor
XX receptor (TNFR) family of polypeptides. PRO364 sequence also shows
XX homology to members of the TNFR family and mouse GTR protein. This clone
XX is assigned the ATCC deposit No: 209436. PRO364 functions as a neoplastic
XX cell growth inhibitor and is used for treating tumours, using an
XX effective amount of PRO655, PRO364 and PRO344. This composition is
XX especially useful for treatment of human cancers such as breast,
XX prostate, colon, lung, renal, ovarian and CNS, leukemia and melanoma
XX
XX Sequence 241 AA;
XX
XX Query Match 56.5%; Score 735.5; DB 3; Length 241;
XX Best Local Similarity 57.0%; Pred. No. 5.8e-60;
XX Matches 134; Conservative 31; Mismatches 61; Indels 9; Gaps 3;
XX
XX QY 1 MGAWMLYGVSMCLVLDLQGPSVVEEPGCGPKGVQSGNNTCCSLYA-----PGKE 53
XX Db 7 MGAFRALCGLALLCALS LGQ-RPTGGPGGPGGELLGTGTDCRCRVTTRCCRDYPGEE 65
XX
XX QY 54 DCPKERCICVTPEYHCGDPQCKICKHYPCQPQQRVESQGDIVGFRFCVACAMGTFSAGRD 113
XX Db 66 CCSEWDCMCVQPFHCGDPCCTTCRHHPCPPGQGVQSGKFSFGFCIDCASGTFSGGHE 125
XX
XX QY 114 GHCLRLWNCISQGFGLTMFGNKNTHNVCIPPELPTQYGHLLTVIFLVMAACIFLLTVQL 173
XX Db 126 GHCKPWTCTQFGFLVFPFGNKNTHNVCVPGSPPAEPLGLWLTVLLVAACVLLLTSAQL 185
XX
XX QY 174 GLHIWQLRRQHMCPRETQPPFAEVLQSAEDACSFQFPPEERGEOT-BEKCHLGGWR 227
XX Db 186 GLHIWQLRSQCMWPRETQLLLEVPPTEDARSQCFPEERGERGSAEKGRLGLDLW 240
XX
XX RESULT 12
XX AAB27651
XX ID AAB27651 standard; protein; 241 AA.
XX

```

```

AC AAB27651;
XX
XX 26-JAN-2001 (first entry)
XX
XX Human protein PRO364.
XX
XX Cardiovascular; endothelial; angiogenic disorder; PRO179; PRO238; PRO364;
XX PRO844; PRO846; PRO1760; PRO205; PRO321; PRO333; PRO840; PRO877; PRO878;
XX PRO879; PRO882; PRO885; PRO887; gene therapy.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..25
XX /label= Signal peptide
XX
XX WO200053757-A2.
XX
XX 14-SEP-2000.
XX
XX 24-FEB-2000; 2000WO-US005004.
XX
XX 08-MAR-1999; 99WO-US005028.
XX 12-MAR-1999; 99US-0123957P.
XX 02-JUN-1999; 99WO-US012252.
XX 20-JUL-1999; 99US-0144758P.
XX 26-JUL-1999; 99US-0145698P.
XX 01-SEP-1999; 99WO-US020111.
XX 15-SEP-1999; 99WO-US021090.
XX 30-NOV-1999; 99WO-US028313.
XX 30-NOV-1999; 99WO-US028409.
XX 02-DEC-1999; 99WO-US028555.
XX 05-JAN-2000; 2000WO-US000219.
XX 18-FEB-2000; 2000WO-US004341.
XX 22-FEB-2000; 2000WO-US004342.
XX 22-FEB-2000; 2000WO-US004414.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Gerritsen ME,
XX Goddard A, Gurney AL, Hillan KJ, Marsters SA, Paoni NP, Pitti RM;
XX Watanabe CK, Williams PM, Wood WI;
XX WPI; 2000-611444/58.
XX N-PSDB; AAA99903.
XX
XX Novel PRO polypeptides and agonists and antagonists of them, used to
XX diagnose and treat cardiovascular, endothelial and angiogenic disorders.
XX
XX Claim 71; Fig 6; 181pp; English.
XX
XX The present invention relates to methods for stimulating or inhibiting
XX angiogenesis and cardiovascularization. The methods involve the use of
XX pharmaceutical compositions based on the following proteins, PRO179,
XX PRO238, PRO364, PRO844, PRO846, PRO1760, PRO205, PRO321, PRO333, PRO840,
XX PRO877, PRO878, PRO879, PRO882, PRO885 or PRO887. These proteins were
XX identified by isolating cDNA clones encoding secreted proteins. The
XX proteins of the invention may be used to diagnose and treat
XX cardiovascular, endothelial or angiogenic disorders. The present sequence
XX is one of the proteins of the invention
XX
XX Sequence 241 AA;
XX
XX Query Match 56.5%; Score 735.5; DB 3; Length 241;
XX Best Local Similarity 57.0%; Pred. No. 5.8e-60;
XX Matches 134; Conservative 31; Mismatches 61; Indels 9; Gaps 3;
XX
XX QY 1 MGAWMLYGVSMCLVLDLQGPSVVEEPGCGPKGVQSGNNTCCSLYA-----PGKE 53
XX Db 7 MGAFRALCGLALLCALS LGQ-RPTGGPGGPGGELLGTGTDCRCRVTTRCCRDYPGEE 65
XX
XX QY 54 DCPKERCICVTPEYHCGDPQCKICKHYPCQPQQRVESQGDIVGFRFCVACAMGTFSAGRD 113
XX ID AAB27651
XX

```


Db 66 CCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGGVQSGKFSFGFCIDCASGTFSGGHE 125
 QY 114 GHCRLLWNCSPQGLTMTFPGNKNTHNAVCIPPELPTQYGHLLTVIFLVMAACIFFLTTVOL 173
 Db 126 GHCKPMTDCTQFGFLTVPFGNKNTHNAVCVPGSPPAEPLGLWLTVLLAVAAACVLLLTSAQL 185
 QY 174 GLHIWQLRQHCMPRETQPPFAEVQLSAEDACSFQFPPEERGEQT-BEKCHLGGRW 227
 Db 186 GLHIWQLRSCQWMPRETQLLLEVPPTEDARSQFPPEERGERSAEKGRLGLDW 240

RESULT 13
 AAY95895
 ID AAY95895 standard; protein; 241 AA.
 XX AAY95895;
 XX 20-NOV-2000 (first entry)
 XX Human tumour necrosis factor receptor-like protein TR11 mutein.
 XX TR11; human; tumour necrosis factor receptor-like protein;
 KW immunodeficiency; autoimmune disease; rheumatoid arthritis;
 KW immunosuppressive; antirheumatic; antiarthritic; haemostatic;
 KW dermatological; antiinflammatory; therapy; diagnosis; mutein; mutant.
 XX Homo sapiens.
 OS
 XX WO200050459-A1.
 XX 31-AUG-2000.
 XX 23-FEB-2000; 2000WO-US004572.
 XX 24-FEB-1999; 99US-0121648P.
 XX 13-MAY-1999; 99US-0134172P.
 XX 16-JUL-1999; 99US-0144076P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Ruben SM, Ni J;
 XX WPI; 2000-572072/53.
 XX Human tumor necrosis factor receptor-like proteins useful for diagnosis,
 PT prevention and treatment of disease states associated with aberrant cell
 PT survival such as autoimmune disease and rheumatoid arthritis.
 XX Disclosure; 294-295; 278pp; English.
 XX The present sequence is that of human tumour necrosis factor receptor-
 CC like protein TR11 (see also AAY95879), a novel protein showing identity
 CC to murine glucocorticoid induced tumour necrosis factor receptor family-
 CC related gene. The invention provides highly conserved TR11, TR11SV1 and
 CC TR11SV2 proteins (see AAY95879-81), as well as vectors, host cells and
 CC recombinant methods for their production. TR11, TR11SV1 and/or TR11SV2
 CC polypeptides are useful for treating, preventing, prognosis and/or
 CC diagnosis of an immunodeficiency, especially common variable
 CC immunodeficiency, X-linked agammaglobulinemia, severe combined
 CC immunodeficiency (SCID), Wiskott-Aldrich syndrome or X-linked
 CC immunoglobulin deficiency with hyper IgM. TR11, TR11SV1 and/or TR11SV2
 CC antagonists (e.g. antibodies) are used to treat, prevent, prognosis and/or
 CC diagnose an autoimmune disease, especially rheumatoid arthritis, systemic
 CC lupus erythematosus, thrombocytopenia purpura or IgA nephropathy. The
 CC polypeptides, polynucleotides and/or antibodies can be administered to
 CC cells in vitro, ex vivo or in vivo or to a multicellular organism.
 CC Soluble forms of the polypeptides may also be used. Methods for screening
 CC for agonist/antagonist compounds are also provided
 XX Sequence 241 AA;
 Query Match 56.5%; Score 735.5; DB 3; Length 241;
 Best Local Similarity 57.0%; Pred. No. 5.8e-60;

Matches 134; Conservative 31; Mismatches 61; Indels 9; Gaps 3;
 QY 1 MCAWMLYGVSMCLVLDLQSPSVVEEPGCGKVGKQVNGNTRCCSLYA-----PGKE 53
 Db 7 MGAFRALCGALCALCALSLQ-Q-RPTGGPGCGPRLLLGTGTDAACCRVHTTRCCRDYPGEE 65
 QY 54 DCPKERCICVTPPEYHCGDPQCCKIKHYPCQPGQGVESQGDIVFGPRCVACAMGTFSSAGRD 113
 Db 66 CCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGGVQSGKFSFGFCIDCASGTFSGGHE 125
 QY 114 GHCRLLWNCSPQGLTMTFPGNKNTHNAVCIPPELPTQYGHLLTVIFLVMAACIFFLTTVOL 173
 Db 126 GHCKPMTDCTQFGFLTVPFGNKNTHNAVCVPGSPPAEPLGLWLTVLLAVAAACVLLLTSAQL 185
 QY 174 GLHIWQLRQHCMPRETQPPFAEVQLSAEDACSFQFPPEERGEQT-BEKCHLGGRW 227
 Db 186 GLHIWQLRSCQWMPRETQLLLEVPPTEDARSQFPPEERGERSAEKGRLGLDW 240

RESULT 14
 AAB24409
 ID AAB24409 standard; protein; 241 AA.
 XX AAB24409;
 XX 07-NOV-2000 (first entry)
 XX Human PRO364 protein sequence SEQ ID NO:117.
 XX Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;
 KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;
 KW angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic;
 KW cytostatic; gene therapy; vaccine.
 XX Homo sapiens.
 OS
 XX WO200032221-A2.
 XX 08-JUN-2000.
 XX 30-NOV-1999; 99WO-US028313.
 XX 01-DEC-1998; 98WO-US025108.
 XX 16-DEC-1998; 98US-0112850P.
 XX 12-JAN-1999; 99US-0115554P.
 XX 08-MAR-1999; 99WO-US005028.
 XX 12-MAR-1999; 99US-0123957P.
 XX 28-APR-1999; 99US-0131445P.
 XX 14-MAY-1999; 99US-0134287P.
 XX 02-JUN-1999; 99WO-US012252.
 XX 23-JUN-1999; 99US-0141037P.
 XX 20-JUL-1999; 99US-0144758P.
 XX 26-JUL-1999; 99US-0145698P.
 XX 01-SEP-1999; 99WO-US020111.
 XX 08-SEP-1999; 99WO-US020594.
 XX 13-SEP-1999; 99WO-US020944.
 XX 15-SEP-1999; 99WO-US021090.
 XX 15-SEP-1999; 99WO-US021547.
 XX 05-OCT-1999; 99WO-US023089.
 XX 29-OCT-1999; 99US-0162506P.
 XX (GETH) GENENTECH INC.
 XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ;
 PI Goddard A, Godowski FJ, Gurney AL, Klein RD, Kuo SS, Paoni NF;
 PI Smith V, Watanabe CK, Williams PM, Wood WI;
 XX WPI; 2000-412154/35.
 XX N-PSDB; AAA77604.
 XX Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing
 PT and treating diagnosing a cardiovascular, endothelial or angiogenic
 PT disorders in mammals.

XX PS Claim 72; Fig 44; 315pp; English.

XX CC The present invention describes nucleic acids encoding PRO polypeptides

XX CC useful for preventing, diagnosing and treating atherosclerosis, and

XX CC cardiovascular, endothelial or angiogenic disorder in mammals by

XX CC modulating cell proliferation, angiogenesis and cardiovascularisation,

XX CC and for identifying agonists and antagonists of these processes. The

XX CC nucleic acids and the proteins they encode may be used in the prevention,

XX CC treatment and diagnosis of diseases associated with inappropriate PRO

XX CC expression such as cardiovascular, endothelial or angiogenic disorders in

XX CC mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For

XX CC example, the nucleic acids (NCs) and vectors containing them and the PRO

XX CC polypeptide may be used to treat disorders associated with decreased PRO

XX CC expression. AAA7510 to AAA7721 and AAB24388 to AAB24435 represent

XX CC nucleotide and protein sequences used in the exemplification of the

XX CC present invention

XX SQ Sequence 241 AA;

Query Match 56.5%; Score 735.5; DB 3; Length 241;

Best Local Similarity 57.0%; Pred. No. 5.8e-60;

Matches 134; Conservative 31; Mismatches 61; Indels 9; Gaps 3;

QY 1 MGAWMLYGVSMCLVLDLQPSVVEEPCGPGKVGQSGNTRCCSLYA-----PGKE 53

DB 7 MGAFRALCGLALLCALSLGQ-RPTGGPGCGPGRLLGTGTDAACRCHVHTTCCRDYPGEE 65

QY 54 DCPKERCICVTPYHCGDPQCKIKHYPCQGORVESQGDIVFGFRCVACAMGTFSGARD 113

DB 66 CCSEWDCMCVQPEFHCGDPCCTTCHRHPCPPGQGVQSKFSGFCQDCASGTFSGGHE 125

QY 114 GHRCLWNTCSQFGFLTMFPFGNKNTHNAVCIPEPLTEQYGHLLTVIFLVMAACIFFLTTVOL 173

DB 126 GHCKPWTDTCTQFGFLTVFPFGNKNTHNAVCPGSPPAEPLGLWTLVLLAAVACVLLLTSAQL 185

QY 174 GLHIWQLRQHMCPRETQFFAEVQLSAEDACSFQFPPEERGGQT-EEKCHLGGRW 227

DB 186 GLHIWQLRSQCMWPRETQLLLEVPSTEDARSQCFPEEERGGERSABEKRLGDLW 240

RESULT 15

AAB47054

ID AAB47054 standard; protein; 241 AA.

XX AAB47054;

XX 08-MAY-2001 (first entry)

XX Human PRO364.

XX PRO364; human; glucocorticoid-induced tumor necrosis factor; receptor;

XX hGTR; ligand; hGTR; PRO175; tumour necrosis factor receptor; TNFR;

XX human umbilical vein endothelial cell; HUVEC; cardiac hypertrophy;

XX myocardial infarction; PGF_2alpha; trauma; cancer; angiogenesis;

XX age-related macular degeneration; antibody; periodontal disease;

XX vascular-related drug targeting; atherosclerosis; hypertension;

XX inflammatory vasculitides; Reynaud's disease; aneurysm;

XX arterial restenosis; thrombophlebitis; tumor angiogenesis; lung; liver;

XX fibrosis; neuropathy; rheumatoid arthritis.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Peptide 1..26

XX Modified-site 146

XX Domain /note= "N-glycosylated"

XX /note= "Potential transmembrane domain"

XX WO200103720-A2.

PD 18-JAN-2001.

XX 11-JUL-2000; 2000MO-US018867.

XX 12-JUL-1999; 99US-0143304P.

XX (GETH) GENENTECH INC.

XX Williams PM, Gerritsen ME;

XX WPI; 2001-138257/14.

XX N-PSDB; AAC85433.

XX Composition for diagnosing and treating cardiovascular, endothelial and

XX PT angiogenic disorders, comprises a PRO364 or PRO175 polypeptide.

XX Claim 1; Fig 1; 76pp; English.

XX This sequence represents PRO364 polypeptide, which is a human gluco-

XX corticoid-induced tumor necrosis factor receptor (hGTR). The

XX corresponding ligand (hGTRL), PRO175, is given in AAB47056. PRO364 and

XX PRO175 may be used in a mixture with a cardiovascular, endothelial,

XX angiogenic or angiostatic agent for the treatment of a cardiovascular,

XX endothelial, angiogenic or angiostatic disorder. The PRO364 cDNA sequence

XX was isolated from an expressed sequence tag (EST) database as having

XX homology to members of the tumor necrosis factor receptor (TNFR) family

XX of polypeptides. The PRO175 cDNA sequence was isolated from a library of

XX cDNA fragments derived from human umbilical vein endothelial cells

XX (HUVEC). Administering an effective amount of PRO364 or PRO175 or their

XX antagonists is useful for treating cardiac hypertrophy (which is

XX initiated by myocardial infarction and characterized by the presence of

XX an elevated level of PGF_2alpha), trauma, a cancer, or age-related

XX macular degeneration in a human. Administering a therapeutically

XX effective amount of an antibody that binds PRO364 or PRO175 is useful for

XX inhibiting angiogenesis induced by PRO364 or PRO175 in a human suffering

XX from a tumor or a retinal disorder. PRO364 or PRO175, or their

XX antagonists, are useful for vascular-related drug targeting or as

XX therapeutic targets for the treatment or prevention of atherosclerosis,

XX hypertension, inflammatory vasculitides, Reynaud's disease, aneurysms,

XX arterial restenosis, thrombophlebitis, tumor angiogenesis, gut protection

XX or regeneration and treatment of lung or liver fibrosis, periodontal

XX diseases, attraction of bone-forming cells, central and peripheral

XX nervous system disease and neuropathies and rheumatoid arthritis

XX SQ Sequence 241 AA;

Query Match 56.5%; Score 735.5; DB 4; Length 241;

Best Local Similarity 57.0%; Pred. No. 5.8e-60;

Matches 134; Conservative 31; Mismatches 61; Indels 9; Gaps 3;

QY 1 MGAWMLYGVSMCLVLDLQPSVVEEPCGPGKVGQSGNTRCCSLYA-----PGKE 53

DB 7 MGAFRALCGLALLCALSLGQ-RPTGGPGCGPGRLLGTGTDAACRCHVHTTCCRDYPGEE 65

QY 54 DCPKERCICVTPYHCGDPQCKIKHYPCQGORVESQGDIVFGFRCVACAMGTFSGARD 113

DB 66 CCSEWDCMCVQPEFHCGDPCCTTCHRHPCPPGQGVQSKFSGFCQDCASGTFSGGHE 125

QY 114 GHRCLWNTCSQFGFLTMFPFGNKNTHNAVCIPEPLTEQYGHLLTVIFLVMAACIFFLTTVOL 173

DB 126 GHCKPWTDTCTQFGFLTVFPFGNKNTHNAVCPGSPPAEPLGLWTLVLLAAVACVLLLTSAQL 185

QY 174 GLHIWQLRQHMCPRETQFFAEVQLSAEDACSFQFPPEERGGQT-EEKCHLGGRW 227

DB 186 GLHIWQLRSQCMWPRETQLLLEVPSTEDARSQCFPEEERGGERSABEKRLGDLW 240

Search completed: October 26, 2005, 15:47:39

Job time : 140.689 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 26, 2005, 15:40:08 ; Search time 28.6823 Seconds
(without alignments)
593.397 Million cell updates/sec

Title: US-09-545-998B-2
Perfect score: 1301
Sequence: 1 MGAWAWLVGVSMCLVDLQ.....PEERGEQTEKCHLGRWP 228

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5A COMB.pep.*
2: /cgn2_6/prodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/prodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/prodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/prodata/1/iaa/6C COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1301	100.0	228	3	US-08-911-423-2
2	1301	100.0	228	4	US-09-512-363-7
3	1301	100.0	228	4	US-09-176-200-7
4	1301	100.0	228	4	US-09-915-593-7
5	735.5	56.5	241	3	US-08-911-423-4
6	735.5	56.5	241	4	US-09-512-363-28
7	735.5	56.5	241	4	US-09-915-593-28
8	735.5	56.5	241	4	US-09-949-016-7232
9	703	54.0	228	3	US-08-911-423-6
10	703	54.0	228	4	US-09-512-363-2
11	703	54.0	234	4	US-09-176-200-2
12	703	54.0	234	4	US-09-915-593-2
13	697	53.6	240	4	US-09-512-363-6
14	697	53.6	240	4	US-09-176-200-6
15	697	53.6	240	4	US-09-915-593-6
16	632.5	48.6	311	3	US-08-911-423-8
17	630.5	48.5	241	4	US-09-512-363-4
18	630.5	48.5	241	4	US-09-176-200-4
19	630.5	48.5	241	4	US-09-915-593-4
20	518	39.8	89	3	US-09-188-930-191
21	518	39.8	89	4	US-09-312-283C-191
22	287	22.1	232	3	US-08-911-423-7
23	228.5	17.6	255	1	US-08-236-918A-8
24	228.5	17.6	255	2	US-08-816-605-9
25	228.5	17.6	255	3	US-09-006-353A-11
26	228.5	17.6	255	3	US-09-007-097-2
27	228.5	17.6	255	3	US-09-150-864A-8

28	228.5	17.6	255	4	US-09-573-986-11	Sequence 11, Appl
29	228.5	17.6	255	4	US-09-578-764A-2	Sequence 2, Appl
30	228.5	17.6	255	4	US-09-623-545A-2	Sequence 2, Appl
31	228.5	17.6	255	5	PCT-US96-03965-8	Sequence 8, Appl
32	228.5	17.6	272	4	US-09-949-016-7520	Sequence 7520, Ap
33	222.5	17.1	219	2	US-08-816-605-2	Sequence 2, Appl
34	203.5	15.6	256	1	US-08-236-918A-6	Sequence 6, Appl
35	203.5	15.6	256	3	US-09-150-864A-6	Sequence 6, Appl
36	203.5	15.6	256	4	US-08-012-269A-2	Sequence 3, Appl
37	203.5	15.6	256	4	US-09-623-545A-3	Sequence 2, Appl
38	203.5	15.6	256	5	PCT-US96-03965-2	Sequence 2, Appl
39	162	12.5	191	3	US-08-974-022-52	Sequence 52, Appl
40	162	12.5	191	3	US-08-795-445A-52	Sequence 52, Appl
41	162	12.5	191	3	US-08-795-447A-52	Sequence 52, Appl
42	162	12.5	191	3	US-08-974-186-52	Sequence 52, Appl
43	162	12.5	191	3	US-08-795-446B-52	Sequence 52, Appl
44	162	12.5	191	3	US-08-706-945D-139	Sequence 139, App
45	162	12.5	191	4	US-08-577-788C-53	Sequence 53, Appl

ALIGNMENTS

RESULT 1
US-08-911-423-2
; Sequence 2, Application US/08911423
; Patent No. 6111090
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Randall, Troy D.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
; TITLE OF INVENTION: REAGENTS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSER: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/911,423
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/023,419
; FILING DATE: 16-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/027,901
; FILING DATE: 07-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0612K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-852-9196
; TELEFAX: 650-496-1200
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 228 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-911-423-2
Query Match 100.0%; Score 1301; DB 3; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.8e-121;

Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGAWAMLYGSMCLVLDLGQPSVVEEPCGPGKVQNGSGNNTCCSLYAPGKEDCPKERC 60
Db 1 MGAWAMLYGSMCLVLDLGQPSVVEEPCGPGKVQNGSGNNTCCSLYAPGKEDCPKERC 60
QY 61 ICVTPEYHCGDPQCKICKHYPCQPGQORVESQGDIVFGFRCVACAMGTFSGAGRDGHCLWT 120
Db 61 ICVTPEYHCGDPQCKICKHYPCQPGQORVESQGDIVFGFRCVACAMGTFSGAGRDGHCLWT 120
QY 121 NCSQFGFLTFMPGNKTHNAVCIPELPTQYGHLTIVFLVMAACIFFLTTLVGLH1WOL 180
Db 121 NCSQFGFLTFMPGNKTHNAVCIPELPTQYGHLTIVFLVMAACIFFLTTLVGLH1WOL 180
QY 181 RQHMCPRETQPPFAEVQLSAEDACSFQFPPEERGEQTEKCHLGGWRP 228
Db 181 RQHMCPRETQPPFAEVQLSAEDACSFQFPPEERGEQTEKCHLGGWRP 228

RESULT 2
US-09-512-363-7
Query Match 100.0%; Score 1301; DB 4; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.8e-121;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
GENERAL INFORMATION:
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins
FILE REFERENCE: PF396
CURRENT FILING DATE: 1997-10-21
EARLIER FILING DATE: 1997-10-21
EARLIER APPLICATION NUMBER: 60/063,212
EARLIER FILING DATE: 1997-10-21
EARLIER APPLICATION NUMBER: 60/176,200
EARLIER FILING DATE: 1998-10-21
EARLIER APPLICATION NUMBER: 60/121,648
EARLIER FILING DATE: 1999-02-24
EARLIER APPLICATION NUMBER: 60/134,172
EARLIER FILING DATE: 1999-05-13
EARLIER APPLICATION NUMBER: 60/144,076
EARLIER FILING DATE: 1999-07-16
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
LENGTH: 228
TYPE: PRT
ORGANISM: Mus musculus
US-09-512-363-7

Query Match 100.0%; Score 1301; DB 4; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.8e-121;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGAWAMLYGSMCLVLDLGQPSVVEEPCGPGKVQNGSGNNTCCSLYAPGKEDCPKERC 60
Db 1 MGAWAMLYGSMCLVLDLGQPSVVEEPCGPGKVQNGSGNNTCCSLYAPGKEDCPKERC 60
QY 61 ICVTPEYHCGDPQCKICKHYPCQPGQORVESQGDIVFGFRCVACAMGTFSGAGRDGHCLWT 120
Db 61 ICVTPEYHCGDPQCKICKHYPCQPGQORVESQGDIVFGFRCVACAMGTFSGAGRDGHCLWT 120
QY 121 NCSQFGFLTFMPGNKTHNAVCIPELPTQYGHLTIVFLVMAACIFFLTTLVGLH1WOL 180
Db 121 NCSQFGFLTFMPGNKTHNAVCIPELPTQYGHLTIVFLVMAACIFFLTTLVGLH1WOL 180
QY 181 RQHMCPRETQPPFAEVQLSAEDACSFQFPPEERGEQTEKCHLGGWRP 228
Db 181 RQHMCPRETQPPFAEVQLSAEDACSFQFPPEERGEQTEKCHLGGWRP 228

RESULT 3
US-09-176-200-7
Sequence 7, Application US/09176200

Patent No. 6509173
GENERAL INFORMATION:
APPLICANT: Ni, Jian
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins
FILE REFERENCE: PF396
CURRENT APPLICATION NUMBER: US/09/176,200
EARLIER FILING DATE: 1998-10-21
EARLIER APPLICATION NUMBER: 60/063,212
EARLIER FILING DATE: 1997-10-21
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
LENGTH: 228
TYPE: PRT
ORGANISM: Mus musculus
US-09-176-200-7
Query Match 100.0%; Score 1301; DB 4; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.8e-121;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGAWAMLYGSMCLVLDLGQPSVVEEPCGPGKVQNGSGNNTCCSLYAPGKEDCPKERC 60
Db 1 MGAWAMLYGSMCLVLDLGQPSVVEEPCGPGKVQNGSGNNTCCSLYAPGKEDCPKERC 60
QY 61 ICVTPEYHCGDPQCKICKHYPCQPGQORVESQGDIVFGFRCVACAMGTFSGAGRDGHCLWT 120
Db 61 ICVTPEYHCGDPQCKICKHYPCQPGQORVESQGDIVFGFRCVACAMGTFSGAGRDGHCLWT 120
QY 121 NCSQFGFLTFMPGNKTHNAVCIPELPTQYGHLTIVFLVMAACIFFLTTLVGLH1WOL 180
Db 121 NCSQFGFLTFMPGNKTHNAVCIPELPTQYGHLTIVFLVMAACIFFLTTLVGLH1WOL 180
QY 181 RQHMCPRETQPPFAEVQLSAEDACSFQFPPEERGEQTEKCHLGGWRP 228
Db 181 RQHMCPRETQPPFAEVQLSAEDACSFQFPPEERGEQTEKCHLGGWRP 228

RESULT 4
US-09-915-593-7
Sequence 7, Application US/09915593
Patent No. 6689607
GENERAL INFORMATION:
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins
FILE REFERENCE: PF396P2
CURRENT APPLICATION NUMBER: US/09/915,593
CURRENT FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: 60/221,577
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 09/512,363
PRIOR FILING DATE: 2000-02-23
PRIOR APPLICATION NUMBER: 60/144,076
PRIOR FILING DATE: 2000-07-16
PRIOR APPLICATION NUMBER: 60/134,172
PRIOR FILING DATE: 1999-05-13
PRIOR APPLICATION NUMBER: 60/121,648
PRIOR FILING DATE: 1999-02-24
PRIOR APPLICATION NUMBER: 09/176,200
PRIOR FILING DATE: 1998-10-21
PRIOR APPLICATION NUMBER: 60/063,212
PRIOR FILING DATE: 1997-10-21
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
LENGTH: 228
TYPE: PRT
ORGANISM: Mus musculus
US-09-915-593-7

Query Match 100.0%; Score 1301; DB 4; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.8e-121;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAWAMLYGVSMCLVLDLQGPSVVEPFGCGPKGVQSGNTRCCSLYA-60
DB 1 MGAWAMLYGVSMCLVLDLQGPSVVEPFGCGPKGVQSGNTRCCSLYA-60

QY 61 ICVTPEYHCGDPCKCKHYPCQPGQORVDSQSDIVFGFRVCACAMGTFSAGRDCHRLWT 120
DB 61 ICVTPEYHCGDPCKCKHYPCQPGQORVDSQSDIVFGFRVCACAMGTFSAGRDCHRLWT 120

QY 121 NCSQFGLTMFPGNKTNAVCIPPELPTQYQGHLLTVIFLVMAACIFPLTTVQLGLHIWOL 180
DB 121 NCSQFGLTMFPGNKTNAVCIPPELPTQYQGHLLTVIFLVMAACIFPLTTVQLGLHIWOL 180

QY 181 RROHMCPRPTOPFAEVQLSAEDACSFQFPEEREGEQTTEKCHLGGWRP 228
DB 181 RROHMCPRPTOPFAEVQLSAEDACSFQFPEEREGEQTTEKCHLGGWRP 228

RESULT 5
US-08-911-423-4
; Sequence 4, Application US/08911423
; Patent No. 611090
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Randall, Troy D.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
; TITLE OF INVENTION: REAGENTS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/911,423
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/023,419
; FILING DATE: 16-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/027,901
; FILING DATE: 07-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0612K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-852-9196
; TELEFAX: 650-496-1200
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 241 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-911-423-4

Query Match 56.5%; Score 735.5; DB 3; Length 241;
Best Local Similarity 57.0%; Pred. No. 3.1e-65;
Matches 134; Conservative 31; Mismatches 61; Indels 9; Gaps 3;

QY 1 MGAWAMLYGVSMCLVLDLQGPSVVEPFGCGPKGVQSGNTRCCSLYA-----PGKE 53
DB 7 MGAFRALCGLALLCALSLGQ-RPTGGPGCGPGRLLLTGTGDARCCRVHTTRCCRDYPGEE 65

QY 54 DCPKERCICVTPEYHCGDPCKCKHYPCQPGQORVDSQSDIVFGFRVCACAMGTFSAGRD 113
DB 66 CCSEWDCMCVQPEFHCGDPCCCTTCRHHPCPPQGVQSGKFSFGFCIDCASGTTFSGGHE 125

QY 114 GHCLRLWNTNCSQFGLTMFPGNKTNAVCIPPELPTQYQGHLLTVIFLVMAACIFPLTTVQL 173
DB 126 GHCKPWTDCQTQFGFLTVFPNKTNAVCVPGSPPAEPLGLWLTVLLVAAACVLLLTSAQL 185

QY 174 GLHIWQLRRQHMCPRETQPPFAEVQLSAEDACSFQFPEEREGEQT-EEKCHLGGWR 227
DB 186 GLHIWQLRRQHMCPRETQPPFAEVQLSAEDACSFQFPEEREGEQT-EEKCHLGGWR 240

RESULT 6
US-09-512-363-28
; Sequence 28, Application US/09512363
; Patent No. 6503184
; GENERAL INFORMATION:
; APPLICANT: N1, Jian
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins
; TITLE OF INVENTION: TR11, TR11SV1, and TR11SV2
; FILE REFERENCE: PF396
; CURRENT APPLICATION NUMBER: US/09/512,363
; CURRENT FILING DATE: 2000-02-23
; EARLIER APPLICATION NUMBER: 60/063,212
; EARLIER FILING DATE: 1997-10-21
; EARLIER APPLICATION NUMBER: 09/176,200
; EARLIER FILING DATE: 1998-10-21
; EARLIER APPLICATION NUMBER: 60/121,648
; EARLIER FILING DATE: 1999-02-24
; EARLIER APPLICATION NUMBER: 60/134,172
; EARLIER FILING DATE: 1999-05-13
; EARLIER APPLICATION NUMBER: 60/144,076
; EARLIER FILING DATE: 1999-07-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-512-363-28

Query Match 56.5%; Score 735.5; DB 4; Length 241;
Best Local Similarity 57.0%; Pred. No. 3.1e-65;
Matches 134; Conservative 31; Mismatches 61; Indels 9; Gaps 3;

QY 1 MGAWAMLYGVSMCLVLDLQGPSVVEPFGCGPKGVQSGNTRCCSLYA-----PGKE 53
DB 7 MGAFRALCGLALLCALSLGQ-RPTGGPGCGPGRLLLTGTGDARCCRVHTTRCCRDYPGEE 65

QY 54 DCPKERCICVTPEYHCGDPCKCKHYPCQPGQORVDSQSDIVFGFRVCACAMGTFSAGRD 113
DB 66 CCSEWDCMCVQPEFHCGDPCCCTTCRHHPCPPQGVQSGKFSFGFCIDCASGTTFSGGHE 125

QY 114 GHCLRLWNTNCSQFGLTMFPGNKTNAVCIPPELPTQYQGHLLTVIFLVMAACIFPLTTVQL 173
DB 126 GHCKPWTDCQTQFGFLTVFPNKTNAVCVPGSPPAEPLGLWLTVLLVAAACVLLLTSAQL 185

QY 174 GLHIWQLRRQHMCPRETQPPFAEVQLSAEDACSFQFPEEREGEQT-EEKCHLGGWR 227
DB 186 GLHIWQLRRQHMCPRETQPPFAEVQLSAEDACSFQFPEEREGEQT-EEKCHLGGWR 240

RESULT 7
US-09-915-593-28
; Sequence 28, Application US/09915593
; Patent No. 6689607

```
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins
; FILE REFERENCE: PF396P2
; CURRENT APPLICATION NUMBER: US/09/915,593
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/221,577
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 09/512,363
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/144,076
; PRIOR FILING DATE: 2000-07-16
; PRIOR APPLICATION NUMBER: 60/134,172
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: 60/121,648
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 09/176,200
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/063,212
; PRIOR FILING DATE: 1997-10-21
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-915-593-28

Query Match      56.5%; Score 735.5; DB 4; Length 241;
Best Local Similarity 57.0%; Pred. No. 3.1e-65;
Matches 134; Conservative 31; Mismatches 61; Indels 9; Gaps 3;

QY 1 MGAWAMLYGVSMLCVLDLGQPSVVEBPGCGKVGKQVSGNNTCCSLYA-----PGKE 53
Db 7 MGAFRALCGLALLCALSLGQ-RPTGGPGCGPGRLLLTGTDAKCRVHTTCCRDYPGEE 65

QY 54 DCPKERCICVTPEYHCGDPQCKICKHYPCQPGQVRVESQGDIVFGPRCVACAMGTFSAGRD 113
Db 66 CCSEWDNCVQPEFHCGDPCCTTCRHHPCCPGQVQSGKSFQCIDCASGTFSGGHE 125

QY 114 GHCLRWNTCSQGFGLTMFPNGKTHNAVCIPEPLPTEQYGHILTVIFLVMAACIFFLTVOL 173
Db 126 GHCKPWTDTQGFGLTVFPNGKTHNAVCPGSPPAEPLGLWLTVLLVAACVLLLTSAQL 185

QY 174 GLHIWQLRRQHCMPRETQPPFAEVOLSAEDACSFQFPPEERGEQT-EKCHLGGRW 227
Db 186 GLHIWQLRSQCMWPRETQLLLEVPPTEDARSQCFPEERGERSAEKGRLGDLW 240

RESULT 8
US-09-949-016-7232
; Sequence 7232, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7232
; LENGTH: 241
; TYPE: PRT
```

```
; ORGANISM: Human
; US-09-949-016-7232

Query Match      56.5%; Score 735.5; DB 4; Length 241;
Best Local Similarity 57.0%; Pred. No. 3.1e-65;
Matches 134; Conservative 31; Mismatches 61; Indels 9; Gaps 3;

QY 1 MGAWAMLYGVSMLCVLDLGQPSVVEBPGCGKVGKQVSGNNTCCSLYA-----PGKE 53
Db 7 MGAFRALCGLALLCALSLGQ-RPTGGPGCGPGRLLLTGTDAKCRVHTTCCRDYPGEE 65

QY 54 DCPKERCICVTPEYHCGDPQCKICKHYPCQPGQVRVESQGDIVFGPRCVACAMGTFSAGRD 113
Db 66 CCSEWDNCVQPEFHCGDPCCTTCRHHPCCPGQVQSGKSFQCIDCASGTFSGGHE 125

QY 114 GHCLRWNTCSQGFGLTMFPNGKTHNAVCIPEPLPTEQYGHILTVIFLVMAACIFFLTVOL 173
Db 126 GHCKPWTDTQGFGLTVFPNGKTHNAVCPGSPPAEPLGLWLTVLLVAACVLLLTSAQL 185

QY 174 GLHIWQLRRQHCMPRETQPPFAEVOLSAEDACSFQFPPEERGEQT-EKCHLGGRW 227
Db 186 GLHIWQLRSQCMWPRETQLLLEVPPTEDARSQCFPEERGERSAEKGRLGDLW 240

RESULT 9
US-08-911-423-6
; Sequence 6, Application US/08911423
; Patent No. 6111090
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Randall, Troy D.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
; TITLE OF INVENTION: REAGENTS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/911,423
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/023,419
; FILING DATE: 16-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/027,901
; FILING DATE: 07-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0612K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-852-9196
; TELEFAX: 650-496-1200
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 228 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-911-423-6
```

Query Match	54.0%;	Score	703;	DB	3;	Length	228;
Best Local Similarity	54.9%;	Pred. No.	5e-62;				
Matches	129;	Conservative	32;	Mismatches	58;	Indels	16;
Gaps	4;						

QY	1	MGAWAMLYGVSMLCVLDLGGQSVVEEPCGPKGVQNGSGNNTRCCSLYA-----PKKE	53
DB	1	MGAFRALCGLALLCALSLGQ-RPTGGPGCGPRLLLGTGTDArcRVHTRCCRDYDGE	59
QY	54	DCPKERCICVTPEYHCGDDPOCKTKYPCQBGQBVESQGDIVGFRCVCACMGCTFSAGRD	113
DB	60	CCSEWDMCVQPFHCGDPCCTCRHHPCPPGQGVQSGKPSFGQCIDCASGTFPSGHE	119
QY	114	GHKRLTNCSQFGFLTMFPGNKTHNACVIPCPLTEQYGHITVFLVMAACIFFLTIVQL	173
DB	120	GHCKPWTDCTQFGFLTVPFGNKTHNACVCPSPAPPLGMLTVLLAAVAAcVLLLTSAQL	179
QY	174	GLHIWLRQHMCPRETQPPFAEVSLSAEDACSGFPPEERGEQT-EKCHILGGHW	227
DB	180	GLHIWLRK-----TOLLLEVPSTEDARSCQFPPEERGERAEKGRIGLDM	227

```

RESULT 10
US-09-512-363-2
; Sequence 2, Application US/09512363
; Patent No. 6503184
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins
; TITLE OF INVENTION: Tr11, Tr11SV1, and Tr11SV2
; FILE REFERENCE: PF396
; CURRENT APPLICATION NUMBER: US/09/512,363
; CURRENT FILING DATE: 2000-02-23
; EARLIER APPLICATION NUMBER: 60/063,212
; EARLIER FILING DATE: 1997-10-21
; EARLIER APPLICATION NUMBER: 09/176,200
; EARLIER FILING DATE: 1998-10-21
; EARLIER APPLICATION NUMBER: 60/121,648
; EARLIER FILING DATE: 1993-02-24
; EARLIER APPLICATION NUMBER: 60/134,172
; EARLIER FILING DATE: 1999-05-13
; EARLIER APPLICATION NUMBER: 60/144,076
; EARLIER FILING DATE: 1999-07-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-512-363-2

```

RESULT 11

```
; ORGANISM: Homo sapiens
US-09-915-593-2

Query Match          54.0%; Score 703; DB 4; Length 234;
Best Local Similarity 54.9%; Pred. No. 5.2e-62;
Matches 129; Conservative 32; Mismatches 58; Indels 16; Gaps 4;

QY 1 MGAWMLYGVSMCLVLDLQGPSVVEEPCGPGKVGKQVSGNNTRCCSLYA-----PKGE 53
Db 7 MGAFAALCGLLALCALSLGQ-RPTGGPGCGPGRLLLTGTDCARCRVHTTRCCRDYPAGL 65

QY 54 DCPKERCICVTPEYHCGDPQCKICKHYPCQGORVESQGDIVFGPRCVACAMGTESAGRD 113
Db 66 CCSEWDCMCVQPEFHCGDPCCTCRHHPCCPGQVQSGKFSFGQCIDCASGTFSGGHE 125

QY 114 GCRLLWNTCSQSGFLTMFPNGKTHNAVCIPEPLTEQYGHLLTVIFLWMAACIFFLTTVQL 173
Db 126 GHCKPWTDTCTQGFGLTVFNGKTHNAVCPGSPPAEPLGWLTVLLAVAAACVLLTSAQL 185

QY 174 GLHIWOLRRQHMCPRETQPPFAEVQLSAEDACSFQPFEEERGEQT-BEKCHLGGRW 227
Db 186 GLHIWOLRK-----TQLLLEVPSTEDARSCQPFEEERGSABEKGRLGDLW 233

RESULT 13
US-09-512-363-6
; Sequence 6, Application US/09512363
; Patent No. 6503184
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins
; FILE REFERENCE: PF396
; CURRENT APPLICATION NUMBER: US/09/512,363
; EARLIER FILING DATE: 2000-02-23
; EARLIER FILING DATE: 1997-10-21
; EARLIER FILING DATE: 1998-10-21
; EARLIER FILING DATE: 1999-02-24
; EARLIER FILING DATE: 1999-05-13
; EARLIER FILING DATE: 1999-07-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 6
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-512-363-6

Query Match          53.6%; Score 697; DB 4; Length 240;
Best Local Similarity 52.2%; Pred. No. 2.1e-61;
Matches 129; Conservative 32; Mismatches 58; Indels 28; Gaps 4;

QY 1 MGAWMLYGVSMCLVLDLQGPSVVEEPCGPGKVGKQVSGNNTRCCSLY-----48
Db 1 MGAFAALCGLLALCALSLGQ-RPTGGPGCGPGRLLLTGTDCARCRVHTTRCCRDYPAGL 59

QY 49 -----APGKEDCPKERCICVTPEYHCGDPQCKICKHYPCQGORVESQGDIVFGRCV 101
Db 60 LGMPVSPCGEECCSWDCMCVQPEFHCGDPCCTCRHHPCCPGQVQSGKFSFGQCI 119

QY 102 ACAMGTFPSAGRDGHCRLWNTCSQGFGLTMFPNGKTHNAVCIPEPLTEQYGHLLTVIFLW 161
Db 120 DCASGTFSGGHEGHCCKPWTDTCTQGFGLTVFNGKTHNAVCPGSPPAEPLGWLTVLLAV 179

QY 162 AACIFPLTTVOLGLHIWOLRRQHMCPRETQPPFAEVQLSAEDACSFQPFEEERGEQT-BEK 220
Db 180 AACVLLTSAQLGLHIWOLRK-----TQLLLEVPSTEDARSCQPFEEERGSABEK 232

RESULT 15
US-09-915-593-6
; Sequence 6, Application US/09915593
; Patent No. 6689607
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins
; FILE REFERENCE: PF396P2
; CURRENT APPLICATION NUMBER: US/09/915,593
; CURRENT FILING DATE: 2001-07-27
; PRIOR FILING DATE: 2000-07-28
; PRIOR FILING DATE: 2000-07-28
; PRIOR FILING DATE: 2000-02-23
; PRIOR FILING DATE: 2000-07-16
; PRIOR FILING DATE: 1999-05-13
```

```
; ORGANISM: Homo sapiens
US-09-915-593-2

Query Match          54.0%; Score 703; DB 4; Length 234;
Best Local Similarity 54.9%; Pred. No. 5.2e-62;
Matches 129; Conservative 32; Mismatches 58; Indels 16; Gaps 4;

QY 1 MGAWMLYGVSMCLVLDLQGPSVVEEPCGPGKVGKQVSGNNTRCCSLYA-----PKGE 53
Db 7 MGAFAALCGLLALCALSLGQ-RPTGGPGCGPGRLLLTGTDCARCRVHTTRCCRDYPAGE 65

QY 54 DCPKERCICVTPEYHCGDPQCKICKHYPCQGORVESQGDIVFGPRCVACAMGTESAGRD 113
Db 66 CCSEWDCMCVQPEFHCGDPCCTCRHHPCCPGQVQSGKFSFGQCIDCASGTFSGGHE 125

QY 114 GCRLLWNTCSQSGFLTMFPNGKTHNAVCIPEPLTEQYGHLLTVIFLWMAACIFFLTTVQL 173
Db 126 GHCKPWTDTCTQGFGLTVFNGKTHNAVCPGSPPAEPLGWLTVLLAVAAACVLLTSAQL 185

QY 174 GLHIWOLRRQHMCPRETQPPFAEVQLSAEDACSFQPFEEERGEQT-BEKCHLGGRW 227
Db 186 GLHIWOLRK-----TQLLLEVPSTEDARSCQPFEEERGSABEKGRLGDLW 233

RESULT 13
US-09-512-363-6
; Sequence 6, Application US/09512363
; Patent No. 6503184
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins
; FILE REFERENCE: PF396
; CURRENT APPLICATION NUMBER: US/09/512,363
; EARLIER FILING DATE: 2000-02-23
; EARLIER FILING DATE: 1997-10-21
; EARLIER FILING DATE: 1998-10-21
; EARLIER FILING DATE: 1999-02-24
; EARLIER FILING DATE: 1999-05-13
; EARLIER FILING DATE: 1999-07-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 6
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-512-363-6

Query Match          53.6%; Score 697; DB 4; Length 240;
Best Local Similarity 52.2%; Pred. No. 2.1e-61;
Matches 129; Conservative 32; Mismatches 58; Indels 28; Gaps 4;

QY 1 MGAWMLYGVSMCLVLDLQGPSVVEEPCGPGKVGKQVSGNNTRCCSLY-----48
Db 1 MGAFAALCGLLALCALSLGQ-RPTGGPGCGPGRLLLTGTDCARCRVHTTRCCRDYPAGL 59

QY 49 -----APGKEDCPKERCICVTPEYHCGDPQCKICKHYPCQGORVESQGDIVFGRCV 101
Db 60 LGMPVSPCGEECCSWDCMCVQPEFHCGDPCCTCRHHPCCPGQVQSGKFSFGQCI 119

QY 102 ACAMGTFPSAGRDGHCRLWNTCSQGFGLTMFPNGKTHNAVCIPEPLTEQYGHLLTVIFLW 161
Db 120 DCASGTFSGGHEGHCCKPWTDTCTQGFGLTVFNGKTHNAVCPGSPPAEPLGWLTVLLAV 179

QY 162 AACIFPLTTVOLGLHIWOLRRQHMCPRETQPPFAEVQLSAEDACSFQPFEEERGEQT-BEK 220
Db 180 AACVLLTSAQLGLHIWOLRK-----TQLLLEVPSTEDARSCQPFEEERGSABEK 232
```



```

; PRIOR APPLICATION NUMBER: 60/121,648
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 09/176,200
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/063,212
; PRIOR FILING DATE: 1997-10-21
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-915-593-6

```

```

Query Match      53.6%; Score 697; DB 4; Length 240;
Best Local Similarity 52.2%; Pred. No. 2.1e-61;
Matches 129; Conservative 32; Mismatches 58; Indels 28; Gaps 4;

QY      1  MGAWAMLYGVSMICVLDLQGPSVVEEPGCGPGKVGQNGSGNTRCCSLY----- 48
Db      1  MGAFRALCGLALLCALUSLGO-RPTGGPGCGGRLLLGTIDARCCRVHTTRCCRDYPAQL 59

QY      49  -----APGKEDCPKERCICVTPEYHCGDPOCKICKHYPCQPGQSVESQGDIVFGRCV 101
Db      60  LGGMPVSCFGECCSEWDCMCVQPEFHGDPCCCTCRHHPCPPGQGVQSQKFSGFQCI 119

QY      102  ACAMGTFSGRDCRLWNCQSGFLTTPPGNKTNAVCIPPLPTEQYGHLTIVFLVM 161
Db      120  DCASGTFSGGHEGCKPWTDTCTQFGLTVFPNGKTNACVCPGSPPAEPLGLWLTVVLLAV 179

QY      162  AACIFELTTVOLGLHTWOLRRQHMCPRETQPPFAEVQLSAEDACSFOPPEERGEQT-EEK 220
Db      180  AACVLLTSAQLGLHIWQURK-----TOLLLEVPSTEDARSCOPPEERGEERSAEK 232

QY      221  CHLGGRW 227
Db      233  GRGLDLW 239

```

Search completed: October 26, 2005, 15:53:37
Job time : 29.6823 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 26, 2005, 15:51:55 ; Search time 109.362 Seconds
(without alignments)
870.278 Million cell updates/sec

Title: US-09-545-998B-2
Perfect score: 1301
Sequence: 1 MGAWMLYGVSMCLVDLGGQ.....PEERGEQTEKCHLGRWP 228

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1862994 seqs, 417510619 residues

Total number of hits satisfying chosen parameters: 1862994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1301	100.0	228	9	US-09-915-593-7
2	1301	100.0	228	13	US-10-116-378-24
3	1301	100.0	228	14	US-10-283-105-7
4	1301	100.0	228	14	US-10-277-966-7
5	1301	100.0	228	17	US-10-959-537-24
6	735.5	56.5	240	16	US-10-783-528-75
7	735.5	56.5	241	9	US-09-915-593-28
8	735.5	56.5	241	13	US-10-116-378-3
9	735.5	56.5	241	14	US-10-283-105-28
10	735.5	56.5	241	14	US-10-277-966-28
11	735.5	56.5	241	15	US-10-295-027-1284

12	735.5	56.5	241	17	US-10-959-537-3
13	735.5	56.5	241	20	US-11-032-294-3
14	703	54.0	234	9	US-09-915-593-2
15	703	54.0	234	14	US-10-283-105-2
16	703	54.0	234	14	US-10-277-966-2
17	697	53.6	240	9	US-09-915-593-6
18	697	53.6	240	14	US-10-283-105-6
19	697	53.6	240	14	US-10-277-966-6
20	697	53.6	246	15	US-10-264-237-1762
21	630.5	48.5	241	9	US-09-915-593-4
22	630.5	48.5	241	14	US-10-283-105-4
23	630.5	48.5	241	14	US-10-277-966-4
24	518	39.8	89	10	US-09-866-050A-191
25	506.5	38.9	317	13	US-10-116-378-26
26	506.5	38.9	317	17	US-10-959-537-26
27	228.5	17.6	255	9	US-09-739-394-9
28	228.5	17.6	255	9	US-09-826-212-11
29	228.5	17.6	255	9	US-09-935-727-13
30	228.5	17.6	255	10	US-09-877-336-2
31	228.5	17.6	255	11	US-09-877-338-2
32	228.5	17.6	255	13	US-10-097-330-9
33	228.5	17.6	255	13	US-10-027-199-2
34	228.5	17.6	255	14	US-10-170-997-2
35	228.5	17.6	255	14	US-10-186-643-11
36	228.5	17.6	255	14	US-10-207-655-160
37	228.5	17.6	255	15	US-10-418-242-13
38	228.5	17.6	255	16	US-10-646-308-18
39	228.5	17.6	255	16	US-10-755-889-174
40	228.5	17.6	255	16	US-10-748-112-15
41	228.5	17.6	255	16	US-10-723-860-588
42	228.5	17.6	255	17	US-10-491-997-32
43	228.5	17.6	255	17	US-10-981-352-2
44	222.5	17.1	219	9	US-09-739-394-2
45	222.5	17.1	219	13	US-10-097-330-2

ALIGNMENTS

RESULT 1
US-09-915-593-7
; Sequence 7, Application US/09915593
; Patent No. US20020098525A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins
; FILE REFERENCE: PFT396P2
; CURRENT APPLICATION NUMBER: US/09/915,593
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/221,577
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 09/512,363
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/144,076
; PRIOR FILING DATE: 2000-07-16
; PRIOR APPLICATION NUMBER: 60/134,172
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: 60/121,648
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 09/176,200
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/063,212
; PRIOR FILING DATE: 1997-10-21
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-915-593-7

```
Query Match      100.0%; Score 1301; DB 9; Length 228;
Best Local Similarity 100.0%; Pred. No. 2.3e-114;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAWAMLYGVSMCLVDLDGQPSVVEEPCGPGKQVNGSGNTRCCSLYAPGKEDCPKERC 60
DB 1 MGAWAMLYGVSMCLVDLDGQPSVVEEPCGPGKQVNGSGNTRCCSLYAPGKEDCPKERC 60

QY 61 ICVTPEYHCGDPQCKICKHYPCQQRVESQGDIVFGFRVCACAMGTFSSAGRDGHCRLWT 120
DB 61 ICVTPEYHCGDPQCKICKHYPCQQRVESQGDIVFGFRVCACAMGTFSSAGRDGHCRLWT 120

QY 121 NCSQFGFLTMFPNGKTHNAVCIPEPLPTEQYGHILTVIFLVMAACIFFLTTLVQLGHLHWL 180
DB 121 NCSQFGFLTMFPNGKTHNAVCIPEPLPTEQYGHILTVIFLVMAACIFFLTTLVQLGHLHWL 180

QY 181 RQHMCPRETQTPFAEVQLSAEDACSFQFPEEREGEQTTEKCHLGGWP 228
DB 181 RQHMCPRETQTPFAEVQLSAEDACSFQFPEEREGEQTTEKCHLGGWP 228

RESULT 2
US-10-116-378-24
; Sequence 24, Application US/10116378
; Publication No. US2002015093A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pitti, Robert M.
; APPLICANT: Wood, William
; TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOG AND
; TITLE OF INVENTION: NUCLEIC
; FILE REFERENCE: P1206R1
; CURRENT APPLICATION NUMBER: US/10/116,378
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-02-09
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-09
; NUMBER OF SEQ ID NOS: 31
; SEQ ID NO 24
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-116-378-24

Query Match      100.0%; Score 1301; DB 13; Length 228;
Best Local Similarity 100.0%; Pred. No. 2.3e-114;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAWAMLYGVSMCLVDLDGQPSVVEEPCGPGKQVNGSGNTRCCSLYAPGKEDCPKERC 60
DB 1 MGAWAMLYGVSMCLVDLDGQPSVVEEPCGPGKQVNGSGNTRCCSLYAPGKEDCPKERC 60

QY 61 ICVTPEYHCGDPQCKICKHYPCQQRVESQGDIVFGFRVCACAMGTFSSAGRDGHCRLWT 120
DB 61 ICVTPEYHCGDPQCKICKHYPCQQRVESQGDIVFGFRVCACAMGTFSSAGRDGHCRLWT 120

QY 121 NCSQFGFLTMFPNGKTHNAVCIPEPLPTEQYGHILTVIFLVMAACIFFLTTLVQLGHLHWL 180
DB 121 NCSQFGFLTMFPNGKTHNAVCIPEPLPTEQYGHILTVIFLVMAACIFFLTTLVQLGHLHWL 180

QY 181 RQHMCPRETQTPFAEVQLSAEDACSFQFPEEREGEQTTEKCHLGGWP 228
DB 181 RQHMCPRETQTPFAEVQLSAEDACSFQFPEEREGEQTTEKCHLGGWP 228

RESULT 3
US-10-283-105-7
; Sequence 7, Application US/10283105
```

```
Publication No. US20030138426A1
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins TR11, TR11SV1,
; FILE REFERENCE: PF396P3
; CURRENT APPLICATION NUMBER: US/10/283,105
; PRIOR FILING DATE: 2002-10-30
; PRIOR APPLICATION NUMBER: 60/330,757
; PRIOR FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 09/915,593
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/221,577
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 09/512,363
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/144,076
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 60/134,172
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: 60/121,648
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 09/176,200
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/063,212
; PRIOR FILING DATE: 1997-10-21
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 228
; TYPE: PRT
; ORGANISM: mus musculus
US-10-283-105-7

Query Match      100.0%; Score 1301; DB 14; Length 228;
Best Local Similarity 100.0%; Pred. No. 2.3e-114;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAWAMLYGVSMCLVDLDGQPSVVEEPCGPGKQVNGSGNTRCCSLYAPGKEDCPKERC 60
DB 1 MGAWAMLYGVSMCLVDLDGQPSVVEEPCGPGKQVNGSGNTRCCSLYAPGKEDCPKERC 60

QY 61 ICVTPEYHCGDPQCKICKHYPCQQRVESQGDIVFGFRVCACAMGTFSSAGRDGHCRLWT 120
DB 61 ICVTPEYHCGDPQCKICKHYPCQQRVESQGDIVFGFRVCACAMGTFSSAGRDGHCRLWT 120

QY 121 NCSQFGFLTMFPNGKTHNAVCIPEPLPTEQYGHILTVIFLVMAACIFFLTTLVQLGHLHWL 180
DB 121 NCSQFGFLTMFPNGKTHNAVCIPEPLPTEQYGHILTVIFLVMAACIFFLTTLVQLGHLHWL 180

QY 181 RQHMCPRETQTPFAEVQLSAEDACSFQFPEEREGEQTTEKCHLGGWP 228
DB 181 RQHMCPRETQTPFAEVQLSAEDACSFQFPEEREGEQTTEKCHLGGWP 228

RESULT 4
US-10-277-966-7
; Sequence 7, Application US/10277966
; Publication No. US20030153499A1
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins TR11, TR11SV2
; FILE REFERENCE: PF396P1D1
; CURRENT APPLICATION NUMBER: US/10/277,966
; PRIOR FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: 09/512,363
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/121,648
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/134,172
```

```

; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: 60/144,076
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/176,200
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/063,212
; PRIOR FILING DATE: 1997-10-21
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 7
; LENGTH: 228
; TYPE: PRT
; ORGANISM: mouse
US-10-277-966-7

Query Match      100.0%; Score 1301; DB 14; Length 228;
Best Local Similarity 100.0%; Pred. No. 2.3e-114;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  MGAWAMLYGVSMCLVDLGGPSVVEBPGCGKVGQSGNNTCCSLYAPGKEDCPKRC 60
DB      1  MGAWAMLYGVSMCLVDLGGPSVVEBPGCGKVGQSGNNTCCSLYAPGKEDCPKRC 60

QY      61  ICVTPEYHCGDPCKICKHYPCQQRVESQGDIVFGFRCVACAMGTFPSAGRDGHCLMT 120
DB      61  ICVTPEYHCGDPCKICKHYPCQQRVESQGDIVFGFRCVACAMGTFPSAGRDGHCLMT 120

QY      121  NCSQFGFLTMFPNGKTHNAVCIPEPLTEQYGHLTWIFLVMAACIFFLTQVGLHQL 180
DB      121  NCSQFGFLTMFPNGKTHNAVCIPEPLTEQYGHLTWIFLVMAACIFFLTQVGLHQL 180

QY      181  RRQHMCPRETQPPFAEVQLSAEDACSFQFPPEERGETECHKLGGRWP 228
DB      181  RRQHMCPRETQPPFAEVQLSAEDACSFQFPPEERGETECHKLGGRWP 228

RESULT 5
US-10-959-537-24
; Sequence 24, Application US/10959537
; Publication No. US20050069983A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pitti, Robert M.
; APPLICANT: Wood, William
; TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOG AND NUCLEIC
; FILE REFERENCE: P1206R1
; CURRENT APPLICATION NUMBER: US/10/959,537
; CURRENT FILING DATE: 2004-10-06
; PRIOR APPLICATION NUMBER: US/09/247,225
; PRIOR FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: US 60/074,087
; PRIOR FILING DATE: 1998-02-09
; NUMBER OF SEQ ID NOS: 31
; SEQ ID NO 24
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-959-537-24

Query Match      100.0%; Score 1301; DB 17; Length 228;
Best Local Similarity 100.0%; Pred. No. 2.3e-114;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  MGAWAMLYGVSMCLVDLGGPSVVEBPGCGKVGQSGNNTCCSLYAPGKEDCPKRC 60
DB      1  MGAWAMLYGVSMCLVDLGGPSVVEBPGCGKVGQSGNNTCCSLYAPGKEDCPKRC 60

QY      61  ICVTPEYHCGDPCKICKHYPCQQRVESQGDIVFGFRCVACAMGTFPSAGRDGHCLMT 120
DB      61  ICVTPEYHCGDPCKICKHYPCQQRVESQGDIVFGFRCVACAMGTFPSAGRDGHCLMT 120

```

```

DB      61  ICVTPEYHCGDPCKICKHYPCQQRVESQGDIVFGFRCVACAMGTFPSAGRDGHCLMT 120
QY      121  NCSQFGFLTMFPNGKTHNAVCIPEPLTEQYGHLTWIFLVMAACIFFLTQVGLHQL 180
DB      121  NCSQFGFLTMFPNGKTHNAVCIPEPLTEQYGHLTWIFLVMAACIFFLTQVGLHQL 180
QY      181  RRQHMCPRETQPPFAEVQLSAEDACSFQFPPEERGETECHKLGGRWP 228
DB      181  RRQHMCPRETQPPFAEVQLSAEDACSFQFPPEERGETECHKLGGRWP 228

RESULT 6
US-10-783-528-75
; Sequence 75, Application US/10783528
; Publication No. US20040219579A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Gish, Kurt
; APPLICANT: Wilson, Keith
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: METHODS OF DIAGNOSIS OF CANCER, COMPOSITIONS AND
; FILE REFERENCE: 05882.0191.NPUS01
; CURRENT APPLICATION NUMBER: US/10/783,528
; CURRENT FILING DATE: 2004-02-19
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 75
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-783-528-75

Query Match      56.5%; Score 735.5; DB 16; Length 240;
Best Local Similarity 57.0%; Pred. No. 5e-61;
Matches 134; Conservative 31; Mismatches 61; Indels 9; Gaps 3;

QY      1  MGAWAMLYGVSMCLVDLGGPSVVEBPGCGKVGQSGNNTCCSLYA-----PGKE 53
DB      7  MGAFRALCGLALLCALSLQ-RPTGGPGCGPGRLLLTGTGDARCCRVHTTRCCRDYPGEE 65

QY      54  DCPKERICVTPEYHCGDPCKICKHYPCQQRVESQGDIVFGFRCVACAMGTFPSAGRD 113
DB      66  CCSEWDCMCVQPEFHCGDPCCCTTCRHPCPPGQGVQSGKFSFGQCIDCASGTFSGGHE 125

QY      114  GHCLRLWNTCSQFGFLTMFPNGKTHNAVCIPEPLTEQYGHLTWIFLVMAACIFFLTQV 173
DB      126  GHCKPMTDCTQFGFLTVFNGKTHNAVCPGSPPAEPLGLWLTVLLAVACVLLLTSAQL 185

QY      174  GLHIWQLRRQHMCPRETQPPFAEVQLSAEDACSFQFPPEERGETECHKLGGRWP 227
DB      186  GLHIWQLRSQCMWPRETQLLLEVPPTEDARSQFPPEERGETECHKLGGRWP 240

RESULT 7
US-09-915-593-28
; Sequence 28, Application US/09915593
; Patent No. US20020098525A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins
; TITLE OF INVENTION: TR11, TR11SV1, and TR11SV2
; FILE REFERENCE: PP396P2
; CURRENT APPLICATION NUMBER: US/09/915,593
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/221,577
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 09/512,363
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/144,076
; PRIOR FILING DATE: 2000-07-16
; PRIOR APPLICATION NUMBER: 60/134,172
; PRIOR FILING DATE: 1999-05-13

```



```

; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1284
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-1284

Query Match          56.5%; Score 735.5; DB 15; Length 241;
Best Local Similarity 57.0%; Pred. No. 5e-61;
Matches 134; Conservative 31; Mismatches 61; Indels 9; Gaps 3;

Qy      1  MGAWAMLYGVSMCLVDLQPSVVVEBPFGCGPKGVQSGNNTCCSLYA-----PGKE 53
Db      7  MGAFRALCGUALCALSLGQ-RTGFGCGCGPGRLLLTGTGDARCCRVHTTRCCRDYFGEE 65

Qy      54  DCPKERCICVTPHYHCGDPQCKTCKHYCPQPGQVRVSQGDIVFGFRVCACAMGTFPSAGRD 113
Db      66  CCSEWDCMCVQPEBFHCGDPCTTCRHHPCPPGQGVQSGKFSFGFQCIDCASGTFSGGHE 125

Qy      114  GHCRLLTNCQSGFLTWPFGNKTHNAVCIPEPLPTQYGHLTWIFLWMAACIFELTTVOL 173
Db      126  GHCKPWTCTQGFGLTVFPGNKTHNAVCFVPGSPPAEPLGLTWLVLLAVAACVLLLTSAQL 185

Qy      174  GLHIWOLRQHMCPRETOPPAEVLQSAEDACSFQFPEERGEOT-BEKCHLGGRW 227
Db      186  GLHIWQLRSOCMPRETQLLLEVPSTEDARSCQFPEERGERSAEBKGLGDLW 240

RESULT 12
US-10-959-537-3
; Sequence 3, Application US/10959537
; Publication No. US20050069983A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pitti, Robert M.
; APPLICANT: Wood, William
; TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOG AND NUCLEOTIDE SEQUENCES ENCODING THE SAME
; FILE REFERENCE: PI206R1
; CURRENT APPLICATION NUMBER: US/10/959,537
; CURRENT FILING DATE: 2004-10-06
; PRIOR APPLICATION NUMBER: US/09/247,225
; PRIOR FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: US 60/074,087
; PRIOR FILING DATE: 1998-02-09
; NUMBER OF SEQ ID NOS: 31
; SEQ ID NO 3
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-959-537-3

```


; PRIOR APPLICATION NUMBER: 60/121,648
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 09/176,200
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/063,212
; PRIOR FILING DATE: 1997-10-21
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 234
; TYPE: PRT
; ORGANISM: human
US-10-283-105-2

Query Match 54.0%; Score 703; DB 14; Length 234;
Best Local Similarity 54.9%; Pred. No. 5.6e-58;
Matches 129; Conservative 32; Mismatches 58; Indels 16; Gaps 4;
QY 1 MGAWMLYGVSMCLVLDLQGPSVVEEPGCGPGKVGQSGNNTCCSLYA-----PGKE 53
Db 7 MGAFRALCGLALLCALSLGQ-RFTGGPGCGPGRLLILGTGTDAECRCRVHTTRCCRDYPGEE 65
QY 54 DCFKERCICVTPYHCGDPQCKICKHYPCQPGQGVESQGDIVFGFRCVACAMGTFSAGRD 113
Db 66 CCSEWDCMCVQPEFHCQDPCTTCRHHPCPPGQGVQSQGKFSFGQCIDCASGTFSGGHE 125
QY 114 GHCLRLWNCQFGLTMTFPGNKTNAVCIPLEPLTPTQYGHLTVIFLVMAACIFPLTTVOL 173
Db 126 GHCKPWTDCQTQFGLTAVFPNGKTHNAVCPVPGSPAPBPLGWLTVVLLAVAAACVLLLTSAOL 185
QY 174 GLHIWLRQHMCPRETQPPAEVQLSAEDACSPQFPEEERGEQT-BEKCHLGGRW 227
Db 186 GLHIWLRK-----TQLLEVPPTEDARSCQFPEEERGERGERSABEKGLGLDLW 233

Search completed: October 26, 2005, 16:11:20
Job time : 111.382 secs

THIS PAGE BLANK

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	228.5	17.6	255	2	I39426	lymphocyte activat
2	203.5	15.6	256	2	B32393	T-cell antigen 4-1
3	134	10.3	272	2	I48700	gene ox40 protein
4	126.5	9.7	271	2	S12783	OX40 antigen precu
5	125.5	9.6	250	1	A49053	CD27 antigen precu
6	122	9.4	277	2	I37552	OX40 homolog - hum
7	119	9.1	1113	2	JE0315	low-density lipopor
8	118.5	9.1	277	2	A60771	B-cell activation
9	115	8.8	435	2	I54182	tumor necrosis fac
10	107.5	8.3	459	2	I48954	gene murine tumour
11	106.5	8.2	474	2	B38634	tumor necrosis fac
12	104.5	8.0	305	2	A46476	B cell-associated
13	102.5	7.9	461	1	A35356	tumor necrosis fac
14	102.5	7.9	1260	1	TVRNRU	protein-tyrosine k
15	102.5	7.9	4543	1	A53102	alpha-2-macroglobu
16	100.5	7.7	1254	2	I48161	p-185 precursor - h
17	100.5	7.7	2321	2	S78549	notch3 protein - h
18	100	7.7	260	1	A46517	CD27 antigen precu
19	99.5	7.6	651	2	JC7705	death receptor-6 -
20	99.5	7.6	1797	2	A55877	laminin beta-2 cha
21	99	7.6	655	2	JC7850	disintegrin and me
22	99	7.6	1964	2	T09059	notch4 - mouse
23	98	7.5	1251	2	A57293	latent transformin
24	95.5	7.3	918	2	JC4361	scavenger receptor
25	95	7.3	344	1	A27701	follistatin precu
26	95	7.3	344	2	A32141	follistatin 1 prec
27	95	7.3	344	2	I45894	follistatin - bovi
28	95	7.3	3635	2	T10053	laminin alpha 5 ch
29	94.5	7.3	329	2	A48805	insulin-like growt

Db 112 QDSSHLKGVDCVPCPPGPHFSGNQACKWTNTCTLSGKQIRHPANSLSLTVCEDRSLAT 171
Qy 142 -----IPE-----PLPTEQYGHLTWIFLWMAACIFLTTVQIG 174
Db 172 LLWETQRTFRPTVTSTTWPRTSOLPSTPLVAEPGPAFAVILGLGLLAPLTVLLA 231
Qy 175 LHIWQLRRQHMCPRETOPAEVQLSADAC---SFQPPSEERGEOTE 218
Db 232 LYL--LRKAWRSNTPKP-----CWGNSFRTPQIE---EQTD 263

RESULT 5
A49053
CD27 antigen precursor - mouse
N;Alternate names: CD27L receptor; T cell activation antigen CD27
C;Species: Mus musculus (house mouse)
C;Date: 19-Dec-1993 #sequence_revision 22-Apr-1995 #text_change 09-Jul-2004
C;Accession: A49053
R;Gravestein, L.A.; Blom, B.; Nolten, L.A.; de Vries, E.; van der Horst, G.; Ossendorp, Eur. J. Immunol. 23, 943-950, 1993
A;Title: Cloning and expression of murine CD27: comparison with 4-1BB, another lymphocyte A;Reference number: A49053; MUID:93209296; PMID:8384562
A;Accession: A49053
A;Molecule type: mRNA
A;Residues: 1-250 <GRA>
A;Cross-references: UNIPROT:P41272
A;Note: sequence extracted from NCBI backbone (NCBIN:128168, NCBI:P128169)
C;Superfamily: CD27 antigen; NGF receptor repeat homology
C;Keywords: duplication; glycoprotein; homodimer; receptor; surface antigen; T-cell; tra F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-250/Product: CD27 antigen #status predicted <MAT>
F;21-182/Domain: extracellular #status predicted <EXT>
F;27-63/Domain: NGF receptor repeat homology <NG1>
F;65-105/Domain: NGF receptor repeat homology <NG2>
F;121-179/Region: proline/serine/threonine-rich
F;183-202/Domain: transmembrane #status predicted <TMN>
F;203-250/Domain: intracellular #status predicted <INT>
F;95,162/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 9.6%; Score 125.5; DB 1; Length 250;
Best Local Similarity 20.8%; Pred. No. 0.0027;
Matches 55; Conservative 30; Mismatches 93; Indels 87; Gaps 13;

Qy 3 AWAMLYGVSMCLVLDLQGPSVVEEPGCGKGVQNGSGNTRCCSLYAPGK---EDCPKER 59
Db 2 AWPPPYWLCMLGTL-VGLSATLAPNSCPDKHYWTGG---LCCRMCEPFGTFVVKDCQDR 57

Qy 60 -----CI---CVTPYHCGDPOCKICKHYPCQPGQGVESQDIVFGFRCVACAMGTF 109
Db 58 TAAQCDCPCIPGTSFSDYHT-RPHCESCRH---CNSGFLIRN-----CTVTANAEC 105

Qy 110 AGRDGHCR-----LWNTCSQFGFLTM 130

Db 106 CSKNWQCRDQECDECDPLNALTQPSSETSPPOPTPLPHGTEKSWPLHRLQPNSTV 165

Qy 131 FPGNKTNAVCIPEPLPT-EQYGHLTWIFLWMAACIFLTTVQIGLHIWQLRRQHMCPRE 189

Db 166 YQSRSSHRPLCSSCIRIFVTFSSMFLIF-VLGAILFF-----HQRRNH----- 208

Qy 190 TOPFAEVQLSADACSFQPPPEERG 214

Db 209 -GPNEDRQAVPEEPCPYSCPREEG 232

RESULT 6
OX40 homolog - human
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: I37552
R;Latza, U.; Durkop, H.; Schnittger, S.; Ringeling, J.; Eitelbach, F.; Hummel, M.; Fonad Eur. J. Immunol. 24, 677-683, 1994

A;Title: The human OX40 homolog: cDNA structure, expression and chromosomal assignment of A;Reference number: I37552; MUID:94170844; PMID:7510240
A;Accession: I37552
A;Status: Preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-277 <RES>
C;Cross-references: UNIPROT:P43489; EMBL:X75962; NID:9472957; PIDN:CAA53576.1; PID:94729; C;Superfamily: CD27 antigen; NGF receptor repeat homology

Query Match 9.4%; Score 122; DB 2; Length 277;
Best Local Similarity 21.1%; Pred. No. 0.0057;
Matches 54; Conservative 22; Mismatches 80; Indels 100; Gaps 8;

Qy 13 LCVLDLQGPSVVEEPGCGKGVQNGSGNTRCCSLYAPGKEDCPKERCICTVTPYHCGDP 72
Db 16 LLLGLGLSTVT-----GLHCVGDTVPSNDRCCHECRPGNGMVR-----CSRS 59

Qy 73 QKCKIKHYPCQPG-----ORVESQDIVF----- 96

Db 60 QNTVCR--PCGPFYNDVVSSKPKCTWCNLRSGSERKQLCTATQDTCRCRAGTQPLD 117

Qy 97 ----GPRVCACAMGTFAGRDGHCRLTWNTCSQFGFLTMFPGNKTNAVCIPEPLTEQYG 152

Db 118 SYKPGVDCAPCPGPHFSPGDNQACKPWTNCTLAKKITLQPASNSDAICEDRPPATQ-- 175

Qy 153 HLTVIPLVMAACITFFLTTLVQLGLHIWQLRRQHMCPRETQ--PFAEVQLSADACSFQFPE 210

Db 176 -----PQETQGPAPRPITVQPTQTEA----WPR 197

Qy 211 HERGEQTEKCHLGGGR 226

Db 198 TSQGPSTRPVEVPGGR 213

RESULT 7
JE0315
Low-density lipoprotein receptor-related protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: JE0315
R;Tomita, Y.; Kim, D.; Magoori, K.; Fujino, T.; Yamamoto, T.T.
J. Biochem. 124, 784-789, 1998
A;Title: A novel low-density lipoprotein receptor-related protein with type II membrane A;Reference number: JE0315; MUID:98429596; PMID:9756624
A;Accession: JE0315
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1113 <TOM>
A;Cross-references: UNIPROT:Q9Z319; DBJ:AB013874; NID:93869144; PIDN:BAA34371.1; PID:938 C;Superfamily: mouse low-density lipoprotein receptor-related protein; LDL receptor ligar F;337-372/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F;374-408/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F;410-445/Domain: LDL receptor ligand-binding repeat homology <LDL3>
F;447-482/Domain: LDL receptor ligand-binding repeat homology <LDL4>
F;648-682/Domain: LDL receptor ligand-binding repeat homology <LDL5>
F;684-720/Domain: LDL receptor ligand-binding repeat homology <LDL6>
F;723-757/Domain: LDL receptor ligand-binding repeat homology <LDL7>
F;869-1097/Domain: trypsin homology <TRY>

Query Match 9.1%; Score 119; DB 2; Length 1113;
Best Local Similarity 25.4%; Pred. No. 0.035;
Matches 75; Conservative 26; Mismatches 96; Indels 98; Gaps 20;

Qy 11 SMLC--VLDLQGPS-----VVEPGCGPGK-----VQNGSGNTRC-----CS 46

Db 390 SLLCDGVDDCGDFSDQNCDCNLTKEHRCGDRGRCIAAEAWVCDGDHD---CVDKSEVNCS 446

Qy 47 LYAPGEDCPKERCICTVTPYHCGDPOCK-----IC--KHYPQCGQGVESQDIVFG 97

Db 447 CHSQGLVECTSGQCIPST--FQCDGDEDCDQSGDEENCSQTPCPGE-----QG--CFG 498

Qy 98 FRCVACAMGTFAGRDGHCRLTWNTCSQFGFLTM-----FPGNKTNAVCI 142

Db 499 SSCVSCAGSSLCDSSSL---SNCSQCEPITILELCLMNLNHYTHYPNVYLGHRTQKEASI 555
QY 143 -----PPLPTQYGHITVIFLVMAACIFPL--TTVOLGLHI--WQLRQHMCPRFTQ 191
Db 556 SWESSLPALVQTCYK-----YLMFFACTILVPKCDVNTQRIIPPCRLLCESKERCES 610
QY 192 PFAEVOLS-AEDACSFOPPEERGEOT-----EE-----KCHLGG 226
Db 611 VLGI VGLQWPEDTDCNQPFEESSDNQTLCLPNEDVEECSPSHFKRSGRCVLGSR 665

RESULT 8
A60771
B-cell activation protein CD40 precursor - human
A:Alternate names: B-cell surface antigen Bp50
C:Species: Homo sapiens (man)
C:Date: 03-Jun-1993 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C:Accession: S04460; A60771
R:Stamenkovic, I.; Clark, E.A.; Seed, B.
EMBO J. 8, 1403-1410, 1989
A:Title: A B-lymphocyte activation molecule related to the nerve growth factor receptor
A:Reference number: S04460; MUID:89356608; PMID:2475341
A:Accession: S04460
A:Molecule type: mRNA
A:Residues: 1-277 <STA>
A:Cross-references: UNIPROT:P25942; EMBL:X60592; NID:G29850; PIDN:CAA43045.1; PID:G29851
R:Braesch-Andersen, S.; Paulie, S.; Koho, H.; Nika, H.; Aspenstroem, P.; Perlmann, P.
J. Immunol. 142, 562-567, 1989
A:Title: Biochemical characteristics and partial amino acid sequence of the receptor-like
A:Reference number: A60771; MUID:89093941; PMID:2463309
A:Accession: A60771
A:Molecule type: protein
A:Residues: 21-50 <BRA>
A:Experimental source: Burkitt lymphoma cell line Raji
C:Genetics:
A:Gene: GDB:CD40
A:Cross-references: GDB:215268; OMIM:109535
A:Map position: 20q12-20q13.2
C:Superfamily: CD27 antigen; NGF receptor repeat homology
C:Keywords: B-cell; glycoprotein; phosphoprotein; surface antigen; transmembrane protein
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-277/Product: B-cell activation protein CD40 #status experimental <MAT>
F:21-193/Domain: extracellular #status predicted <EXT>
F:194-215/Domain: transmembrane #status predicted <TM>
F:216-277/Domain: intracellular #status predicted <CYT>
F:153,180/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 9.1%; Score 118.5; DB 2; Length 277;
Best Local Similarity 21.0%; Pred. No. 0.011; Mismatches 88; Indels 71; Gaps 10;
Matches 50; Conservative 29

QY 41 NTRCCSLYAPGKE---DCPK-----ERC----- 60
Db 34 NSQCCSLCPGGKLVSDCTFTETECPCGESEFLDTWNRTHCHQHKYCDPNLGLRVQ 93

QY 61 -----ICVTPE-VHCGDPQCKIC-KHYPCQPGQGVESQGDIVPGFPFCVACAMGTFPS- 109
Db 94 KGTSETDTICTCEGWHCTSEACESCVLHRSKSPGFGVKQIATGVSDDTICEPCPVGFFSN 153

QY 110 -AGRDGHCHLWNTCSQFGLTFPPGKNKTNVACIPELPLETQYGHITVIFLVMAACIFPL 168
Db 154 VSAAFEKHPWTSCTEYKDLIVVQAGNKTDDVVGPPQ-----DLRALVPIPIF-GILFAI 208

QY 169 TTVOLGLHIWQLRRQHMCPRFTQPFPAEVOLSABDACSFQFPEERGEOT-----EEKCH 222
Db 209 LLVLVFIKKVAKPTNKAFHPKQEPQEI-----NFPDDLPGSNTAAPVQETLH 256

RESULT 9
I54182
tumor necrosis factor receptor 2-related protein - human
C:Species: Homo sapiens (man)
C:Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004

C:Accession: I54182
R:Baens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.
Genomics 16, 214-218, 1993
A:Title: Construction and evaluation of a hncDNA library of human 12p transcribed sequenc
A:Reference number: I54182; MUID:93252381; PMID:8486360
A:Accession: I54182
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-435 <RES>
A:Cross-references: UNIPROT:P36941; GB:I04270; NID:G339761; PIDN:AAA36757.1; PID:G339762
C:Genetics:
A:Gene: GDB:LTBR
A:Cross-references: GDB:1230195; OMIM:600979
A:Map position: 12p13.3-12p13.1
C:Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolo

Query Match 8.8%; Score 115; DB 2; Length 435;
Best Local Similarity 22.2%; Pred. No. 0.033; Mismatches 54; Conservative 23; Indels 72; Gaps 13;
Matches 54

QY 3 AWAMLYGVSMCLVDLGGPSVY-----EPPGCGPGKQVNGSGNNTCCSLYAPG---KED 54
Db 13 AWGPLV-LGLFGLLAASQPAVPPYASENQTCRDQKEYYEPQHRRICCSRCPPGTVSAAK 71

QY 55 CPKER-CICVTPEYHCG-----DP-----OCKI- 76
Db 72 CSRIRDTVCAT-----CAENSYNEHWNLYITICQLRCPDPVVMGLEIAPCTSKRKTQCRQ 127

QY 77 -----CKH-----YPCQPGQGVESQGDIVFG-FRCVACAMGTF---SAGRDGHCHRL 118
Db 128 PQMFCAAWALECTHCELLSDCPGTEAEKLDKDEVGKNNHCVPCKAGHFQNTSSPSARCP 187

QY 119 WTNCSQFGFLTMFPGNKTHNAVCIIP--EPLPTEQYGHITVIFLVMAACIFLTTVOLGLH 176
Db 188 HTRCENQGLVEAAPGTAQSDTTCKNPLEPLPEMSGTW-LMLAVLLPLAFLLLATVFSC 246

QY 177 IWQ 179
Db 247 IWK 249

RESULT 10
I48854
gene murine tumour necrosis factor receptor 2 protein - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I48854
R:Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.
Mamm. Genome 5, 726-727, 1994
A:Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.
A:Reference number: I48854; MUID:95178848; PMID:7873884
A:Accession: I48854
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-459 <RES>
A:Cross-references: UNIPROT:Q62327; EMBL:X76401; NID:G433830; PIDN:CAA53981.1; PID:G43383;
C:Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homolo
F:151-188/Domain: NGF receptor repeat homology <NGF>

Query Match 8.3%; Score 107.5; DB 2; Length 459;
Best Local Similarity 26.1%; Pred. No. 0.14; Mismatches 13; Indels 77; Gaps 13;
Matches 54; Conservative 13

QY 4 WAMLYGVSMCLVDLGGPSVVEEPG-----CGPGKQVNGSGNNT- 42
Db 2 WATGHTVPAQVVLTPYKP---EPGYEQIISQYYDRKAQMCCKACPPQGYVKHFCKNKT 57

QY 43 -----RCCSLYAPGKE-----CPKER---CICVTPEY-----H 68
Db 58 DTVCADCEASMYTQVMNQFRCTLSCSSSCSTDQVTRACTKQONRVCAACEAGRYCALKTH 117

QY 69 CGDPCKICKHY-PCQPGQGVES-----QGDIVFGFRCVACAMGTFPS--AGRDGHCHRLWNT 121

Db 118 SG--SCRCQWRLSKCGFGVASSRAPNGVNL-----CKACAPGTFSDTTSTSDVCRPHRI 171

QY 122 CSQFGFLTMFPNGKTNHNAVCIPEPLPT 148

Db 172 CS-----ILAIPGNASTDAVCAPES-PT 193

RESULT 11

B38634

tumor necrosis factor receptor type 2 precursor - mouse

C;Species: Mus musculus (house mouse)

C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004

C;Accession: B38634; A40254; S54816

R;Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E.

Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991

A;Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor

A;Reference number: A38634; MUID:91187885; PMID:1849278

A;Accession: B38634

A;Molecule type: mRNA

A;Residues: 1-474 <LEW>

A;Cross-references: UNIPROT:P25119; GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828

R;Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jenk

Mol. Cell. Biol. 11, 3020-3026, 1991

A;Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for

A;Reference number: A40254; MUID:91246168; PMID:1645445

A;Accession: A40254

A;Molecule type: mRNA

A;Residues: 1-474 <GOO>

A;Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828

R;Kisssoneghis, M.; Fallowes, R.; Feldmann, M.; Chernajovsky, Y.

submitted to the EMBL Data Library, May 1995

A;Description: Characterization of the promoter region of the murine p75-TNF receptor.

A;Reference number: S54816

A;Accession: S54816

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-22 <KTS>

A;Cross-references: EMBL:X87128; NID:g809043; PIDN:CAA60618.1; PID:g809044

C;Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homolo

C;Keywords: cytokine receptor; transmembrane protein

F;1-22/Domain: signal sequence #status predicted <SIG>

F;23-474/Product: tumor necrosis factor receptor type 2 #status predicted <MAT>

F;40-77/Domain: NGF receptor repeat homology <NG1>

F;79-120/Domain: NGF receptor repeat homology <NG2>

F;166-203/Domain: NGF receptor repeat homology <NG4>

Query Match 8.2%; Score 106.5; DB 2; Length 474;

Best Local Similarity 26.1%; Pred. No. 0.18;

Matches 54; Conservative 13; Mismatches 63; Indels 77; Gaps 13;

QY 4 WAMLYGVSMLCVLDLGQPSVVEBPG-----CGPGKVQNGSGNNT- 42

Db 17 WATGHTVPAQVLTTPYKP----EPGYECQISOEYYDRKAQCCAKCPGQVVFHFCNKTS 72

QY 43 -----RCCSLYAPGKED-----CPKER---CICVTPEY-----H 68

Db 73 DTVCADCEASMYTQVWNOFTCLSCSSCTTDQVEIRACTQKQNRVCAEAGRYCALKTH 132

QY 69 CGDPQCKICKHY-PCQPGQRVES-----QGDIVFGFRCVACAMGTFS--AGRDGHCRLMTN 121

Db 133 SG--SCRCQWRLSKCGFGVASSRAPNGVNL-----CKACAPGTFSDTTSTSDVCRPHRI 186

QY 122 CSQFGFLTMFPNGKTNHNAVCIPEPLPT 148

Db 187 CS-----ILAIPGNASTDAVCAPES-PT 208

RESULT 12

A46476

B cell-associated surface molecule CD40, long splice form - mouse

C;Species: Mus musculus (house mouse)

C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C;Accession: A46476; A46515

R;Torres, R.M.; Clark, E.A.

J. Immunol. 148, 620-626, 1992

A;Title: Differential increase of an alternatively polyadenylated mRNA species of murine

A;Reference number: A46476; MUID:92105763; PMID:1370315

A;Accession: A46476

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-305 <TOR>

A;Cross-references: UNIPROT:P27512; GB:M83312; NID:g1553058

A;Note: sequence extracted from NCBI backbone (NCBIN:75206, NCBIP:75207)

A;Note: this translation is not annotated in GenBank entry MUSCD40A, release 113.0

R;Grimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Cockayne,

J. Immunol. 149, 3921-3926, 1992

A;Title: Genomic structure and chromosomal mapping of the murine CD40 gene.

A;Reference number: A46515; MUID:93094586; PMID:1281194

A;Accession: A46515

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: nucleic acid

A;Residues: 1-287, 'IV' <GRI>

A;Cross-references: GB:M83312; NID:g1553058; PIDN:AA808705.1; PID:g1553059; GB:M94126; N1

A;Experimental source: BALB/c, liver

A;Note: sequence extracted from NCBI backbone (NCBIP:120357)

C;Comment: For an alternative splice form, see PIR:A46515.

C;Comment: For an alternative splice form, see PIR:A46476.

C;Superfamily: CD27 antigen; NGF receptor repeat homology

C;Keywords: alternative splicing; transmembrane protein

F;105-144/Domain: NGF receptor repeat homology <NGF>

Query Match 8.0%; Score 104.5; DB 2; Length 305;

Best Local Similarity 25.2%; Pred. No. 0.18;

Matches 38; Conservative 13; Mismatches 71; Indels 29; Gaps 8;

QY 17 DLGQP-----SVVEBPGCGP---GKVQNGSGNNTRC-----CSLYAPG-----KED 54

Db 39 DLCPGSRLLTSHCTALEKTCQCHPCDSEFSAQWNRIRCHQHRHCE---PNOGLRVKKG 95

QY 55 CPKERCICVTPE-YHCGDPQKTC-KHYPCQPGQRVESQGDIVFGFRCVACAMGTFS--A 110

Db 96 TAESDVTCTCKEQHCTSKDCEACQHTPCIPGFGVEMEMATETDTVCHPCPVGFFSNQS 155

QY 111 GRDGHRLWTNCSQFGFLTMFPNGKTNHNAV 141

Db 156 SLPEKCYPTWTSCEBCKNLEVLQKGTSTQTNVIC 186

RESULT 13

A35356

tumor necrosis factor receptor 2 precursor [validated] - human

N;Alternate names: 75K tumor necrosis factor receptor; TNF receptor type 2

C;Species: Homo sapiens (man)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C;Accession: A35356; A36475; A48416; A36007; A23666; B35010; I38094

R;Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower, S.K.

Science 248, 1019-1023, 1990

A;Title: A receptor for tumor necrosis factor defines an unusual family of cellular and

A;Reference number: A35356; MUID:90260639; PMID:2160731

A;Accession: A35356

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-461 <SMI>

A;Cross-references: UNIPROT:P20333; GB:M32315; NID:g189185; PIDN:AAA59929.1; PID:g189186

R;Kohn, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squires,

Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990

A;Title: A second tumor necrosis factor receptor gene product can shed a naturally occur

A;Reference number: A36475; MUID:91045991; PMID:2172983

A;Accession: A36475

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-195, 'R', 197-461 <KOH>

A;Cross-references: GB:M55994; GB:M38549; NID:g339757; PIDN:AAA36755.1; PID:g339758

R;Dembic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus, M.;

Cytokine 2, 231-237, 1990

A;Title: Two human TNF receptors have similar extracellular, but distinct intracellular,

A:Reference number: A48416; MUID:91370690; PMID:1966549

A:Accession: A48416

A>Status: preliminary

A:Molecule type: mRNA; protein

A:Residues: 23-461 <DEM>

A:Cross-references: GB:S63368; NID:9235648; PIDN:AAAB19824.1; PID:9235649

A>Note: sequence extracted from NCBI backbone (NCBIN:63368, NCBIP:63371)

R:Hellier, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M.

Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990

A:Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demonstration of its role in tumor necrosis factor-induced apoptosis

A:Reference number: A36007; MUID:90349572; PMID:2166946

A:Accession: A36007

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 116-140, 'P', '142-195, 'R', '197-362, 'T', '364-461 <HEI>

A:Cross-references: GB:M35857; NID:9339751; PIDN:AAAG3262.1; PID:9339752

R:Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M.

J. Biol. Chem. 265, 20131-20138, 1990

A:Title: Purification and partial amino acid sequence analysis of two distinct tumor necrosis factor receptors

A:Reference number: A23666; MUID:91056048; PMID:2173696

A:Accession: A23666

A>Status: preliminary

A:Molecule type: protein

A:Residues: 23-40; 65-69; 136-141; 300-306 <LOE>

R:Engelmann, H.; Novick, D.; Wallach, D.

J. Biol. Chem. 265, 1531-1536, 1990

A:Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence for two distinct receptors

A:Reference number: A35010; MUID:90110215; PMID:2153136

A:Accession: B35010

A>Status: preliminary

A:Molecule type: protein

A:Residues: 27-31 <ENG>

R:Kuhnert, P.; Kemper, O.; Wallach, D.

Gene 150, 381-386, 1994

A:Title: Cloning, sequencing and partial functional characterization of the 5' region of the human TNF receptor

A:Reference number: I38094; MUID:95121934; PMID:7821811

A:Accession: I38094

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-37 <RES>

A:Cross-references: EMBL:X80021; NID:g666044; PIDN:CAA56324.1; PID:g825701

C:Genetics:

A:Gene: GDB:TNFR2

A:Cross-references: GDB:125914; OMIM:191191

A:Map position: lp36.2-1p36.2

A:Introns: 26/3

A>Note: the list of introns is incomplete

C:Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homology

C:Keywords: duplication; glycoprotein; receptor; transmembrane protein

F:1-22/Domain: signal sequence #status predicted <SIG>

F:23-416/Product: tumor necrosis factor receptor 2 #status experimental <MAT>

F:40-76/Domain: NGF receptor repeat homology <NG1>

F:78-119/Domain: NGF receptor repeat homology <NG2>

F:120-162/Domain: NGF receptor repeat homology <NG3>

F:164-201/Domain: NGF receptor repeat homology <NG4>

F:262-279/Domain: transmembrane #status predicted <TMN>

F:280-461/Domain: intracellular #status predicted <INT>

F:171,193/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 7.9%; Score 102.5; DB 1; Length 461;

Best Local Similarity 22.4%; Pred. No. 0.38;

Matches 52; Conservative 18; Mismatches 67; Indels 95; Gaps 12;

QY 29 CGPG---KVQNGSGNNTRC-----CSLYAPGKEDCPKER-- 59

Db 57 CSPGQAKVFCYTKSTDTVCDSCEDSTYTLQWVWPFLCSGSRCSDDQVETQACTREQNR 116

QY 60 -CICVTPYHCG---DPQCKICKHY-PCQPGQVRSQGDIVFGFRVCVACMGTFSS--AGR 112

Db 117 ICTC-RPGWYCALSKQEGCRCLCAPLRCRPGFGVARGPTGSDVVCPCAPGTFSTSS 175

QY 113 DGHCLRWTCNSQGFGLTMFPGNKTHNVC-----IPEPLTEQYGHLYVI 157

(

Db 176 TDICRPHOICN----VVAIPGNASMDVACTSTSPTRSMAPGAVHLPQPVST----- 222

QY 158 FLVMAACIFFLTTLVQLGLHIMQLRRQHMCPRETQPPFAEVQLSAEDACSFQFP 209

Db 223 -----RSQH-----TQPTPEP--STADSTSLFLP 244

RESULT 14

TVRTNU

C:Species: Rattus norvegicus (Norway rat)

C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004

C:Accession: A24562; A61204

R:Bargmann, C.I.; Hung, M.C.; Weinberg, R.A.

Nature 319, 226-230, 1986

A:Title: The new oncogene encodes an epidermal growth factor receptor-related protein.

A:Reference number: A34562; MUID:86118662; PMID:3945311

A:Accession: A24562

A:Molecule type: mRNA

A:Residues: 1-1260 <BAR>

A:Cross-references: UNIPROT:P06494; EMBL:X03362; NID:g56745; PIDN:CAA27059.1; PID:g56746

R:Masui, T.; Mann, A.M.; Macatee, T.L.; Garland, E.M.; Okamura, T.; Smith, R.A.; Cohen, E.

Carcinogenesis 12, 1975-1978, 1991

A:Title: Direct DNA sequencing of the rat neu oncogene transmembrane domain reveals no m

2-thiazolylformamide or N-methyl-N-nitrosourea.

A:Reference number: A61204; MUID:92035293; PMID:1682063

A:Accession: A61204

A:Molecule type: DNA

A:Residues: 637-663, 'V', '665-702 <MAS>

A>Note: authors translated the codon GCA for residue 25 as Val

C:Genetics:

A:Gene: neu

C:Superfamily: epidermal growth factor receptor; protein kinase homology

C:Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphoprotein; phosphot

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-1260/Product: protein-tyrosine kinase neu #status predicted <MAT>

F:658-680/Domain: transmembrane #status predicted <TMN>

F:723-988/Domain: protein kinase ATP-binding motif

F:731-739/Region: protein kinase ATP-binding motif

F:71,191,263,535,576,634/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:691/Binding site: phosphate (Thr) (covalent) #status predicted

F:758/Active site: Lys #status predicted (Tyr) (covalent) #status predicted

F:882,1227,1253/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 7.9%; Score 102.5; DB 1; Length 1260;

Best Local Similarity 26.6%; Pred. No. 0.92;

Matches 46; Conservative 21; Mismatches 73; Indels 33; Gaps 9;

QY 30 GPGKVQNGSGNNTRC--CSLYAPGKEDCPKERICVTPYHCGDPCCKICKHYPCQPGQR 87

Db 527 GGGP-----TQCWNGSHFLRGQECVEECRWKGLPREYVSDKRLCLPC-HPECCP--- 574

QY 88 VESQGDIVFGF---RCVACAMGTESAGRDGHC-----RLWTNCSQFGFLTMFPG 133

Db 575 -QNSSETCFGSEADQCAAHYKDSVSCVVARCPGSKPDLSPMPWKYDEEGICQCPFI 633

QY 134 NKTHNAVCIPE--PLPTEQYGH--LTVIFLVMAACIFFLTTLVQLGLHIMQLRRQ 183

Db 634 NCTHSCVDLDERGCPAEQASRPVTFIATVEGVLFLILVVVVVGILJ-KRRRQ 685

RESULT 15

AS3102

alpha-2-macroglobulin receptor precursor - chicken

N:Alternate names: CD91; LDL receptor-related protein 1; low density lipoprotein receptor

C:Species: Gallus gallus (chicken)

C:Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 09-Jul-2004

C:Accession: A53102

R:Nimf, J.; Stifani, S.; Bilous, P.T.; Schneider, W.J.

J. Biol. Chem. 269, 212-219, 1994

A:Title: The somatic cell-specific low density lipoprotein receptor-related protein of th

A:Reference number: A53102; MUID:94103212; PMID:7506255

A:Accession: A53102
A:Status: Preliminary
A:Molecule type: mRNA
A:Residue: 1-4543 <NIM>
A:Cross-references: UNIPROT:P98157; GB:X74904; NID:G438006; PIDN:CAA52870.1; PID:G438007
C:Complex: The alpha-2-macroglobulin receptor complex consists of noncovalently-associated d protein.
C:Superfamily: alpha-2-macroglobulin receptor; EGF homology; LDL receptor ligand-binding
C:Keywords: Beta-hydroxyaspartate; beta-hydroxyaspartic acid; calcium binding; glycoprotein
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-3942/Domain: alpha-2-macroglobulin receptor 515K chain #status predicted <515K>
F:18-3942,3943-4543/Product: alpha-2-macroglobulin receptor #status predicted <MAT>
F:29-66/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F:74-110/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F:117-150/Domain: EGF homology <EG1>
F:156-190/Domain: EGF homology <EG2>
F:200-241/Domain: LDL receptor YWTD-containing repeat homology <YW01>
F:242-283/Domain: LDL receptor YWTD-containing repeat homology <YW02>
F:294-336/Domain: LDL receptor YWTD-containing repeat homology <YW03>
F:337-380/Domain: LDL receptor YWTD-containing repeat homology <YW04>
F:381-422/Domain: LDL receptor YWTD-containing repeat homology <YW05>
F:423-470/Domain: LDL receptor YWTD-containing repeat homology <YW06>
F:480-521/Domain: EGF homology <EG3>
F:573-615/Domain: LDL receptor YWTD-containing repeat homology <YW07>
F:616-661/Domain: LDL receptor YWTD-containing repeat homology <YW08>
F:662-712/Domain: LDL receptor YWTD-containing repeat homology <YW09>
F:713-754/Domain: LDL receptor YWTD-containing repeat homology <YW10>
F:755-797/Domain: LDL receptor YWTD-containing repeat homology <YW11>
F:805-840/Domain: EGF homology <EG4>
F:852-888/Domain: LDL receptor ligand-binding repeat homology <LDL3>
F:893-929/Domain: LDL receptor ligand-binding repeat homology <LDL4>
F:934-969/Domain: LDL receptor ligand-binding repeat homology <LDL5>
F:974-1009/Domain: LDL receptor ligand-binding repeat homology <LDL6>
F:1013-1049/Domain: LDL receptor ligand-binding repeat homology <LDL7>
F:1060-1095/Domain: LDL receptor ligand-binding repeat homology <LDL8>
F:1102-1138/Domain: LDL receptor ligand-binding repeat homology <LDL9>
F:1143-1180/Domain: LDL receptor ligand-binding repeat homology <LDLA>
F:1183-1219/Domain: EGF homology <EG5>
F:1225-1259/Domain: EGF homology <EG6>
F:1267-1306/Domain: LDL receptor YWTD-containing repeat homology <YW12>
F:1307-1353/Domain: LDL receptor YWTD-containing repeat homology <YW13>
F:1354-1396/Domain: LDL receptor YWTD-containing repeat homology <YW14>
F:1397-1443/Domain: LDL receptor YWTD-containing repeat homology <YW15>
F:1444-1486/Domain: LDL receptor YWTD-containing repeat homology <YW16>
F:1487-1529/Domain: LDL receptor YWTD-containing repeat homology <YW17>
F:1538-1576/Domain: EGF homology <EG7>
F:1581-1624/Domain: LDL receptor YWTD-containing repeat homology <YW18>
F:1625-1667/Domain: LDL receptor YWTD-containing repeat homology <YW19>
F:1668-1711/Domain: LDL receptor YWTD-containing repeat homology <YW20>
F:1712-1751/Domain: LDL receptor YWTD-containing repeat homology <YW21>
F:1752-1794/Domain: LDL receptor YWTD-containing repeat homology <YW22>
F:1795-1842/Domain: LDL receptor YWTD-containing repeat homology <YW23>
F:1846-1882/Domain: EGF homology <EG8>
F:1930-1972/Domain: LDL receptor YWTD-containing repeat homology <YW24>
F:1973-2015/Domain: LDL receptor YWTD-containing repeat homology <YW25>
F:2016-2059/Domain: LDL receptor YWTD-containing repeat homology <YW26>
F:2060-2101/Domain: LDL receptor YWTD-containing repeat homology <YW27>
F:2102-2147/Domain: LDL receptor YWTD-containing repeat homology <YW28>
F:2155-2196/Domain: EGF homology <EG9>
F:2195-2237/Domain: LDL receptor YWTD-containing repeat homology <YW29>
F:2247-2288/Domain: LDL receptor YWTD-containing repeat homology <YW30>
F:2338-2382/Domain: LDL receptor YWTD-containing repeat homology <YW31>
F:2424-2467/Domain: LDL receptor YWTD-containing repeat homology <YW32>
F:2476-2511/Domain: EGF homology <EG10>
F:2518-2555/Domain: LDL receptor ligand-binding repeat homology <LDLB>
F:2560-2594/Domain: LDL receptor ligand-binding repeat homology <LDLC>
F:2599-2633/Domain: LDL receptor ligand-binding repeat homology <LDLD>
F:2646-2682/Domain: LDL receptor ligand-binding repeat homology <LDLE>
F:2690-2724/Domain: LDL receptor ligand-binding repeat homology <LDLF>
F:2732-2767/Domain: LDL receptor ligand-binding repeat homology <LDLG>
F:2772-2810/Domain: LDL receptor ligand-binding repeat homology <LDLH>
F:2816-2851/Domain: LDL receptor ligand-binding repeat homology <LDLI>

F:2856-2895/Domain: LDL receptor ligand-binding repeat homology <LDLJ>
F:2902-2936/Domain: LDL receptor ligand-binding repeat homology <LDLK>
F:2941-2977/Domain: EGF homology <EG11>
F:2983-3018/Domain: EGF homology <EG12>
F:3026-3065/Domain: LDL receptor YWTD-containing repeat homology <YW34>
F:3066-3110/Domain: LDL receptor YWTD-containing repeat homology <YW35>
F:3111-3153/Domain: LDL receptor YWTD-containing repeat homology <YW36>
F:3154-3197/Domain: LDL receptor YWTD-containing repeat homology <YW37>
F:3198-3238/Domain: LDL receptor YWTD-containing repeat homology <YW38>
F:3239-3281/Domain: LDL receptor YWTD-containing repeat homology <YW39>
F:3291-3327/Domain: EGF homology <EG13>
F:3331-3366/Domain: LDL receptor ligand-binding repeat homology <LDLL>
F:3371-3405/Domain: LDL receptor ligand-binding repeat homology <LDLM>
F:3410-3445/Domain: LDL receptor ligand-binding repeat homology <LDLN>
F:3450-3486/Domain: LDL receptor ligand-binding repeat homology <LDLO>
F:3491-3528/Domain: LDL receptor ligand-binding repeat homology <LDLP>
F:3533-3567/Domain: LDL receptor ligand-binding repeat homology <LDLQ>
F:3572-3606/Domain: LDL receptor ligand-binding repeat homology <LDLR>
F:3610-3644/Domain: LDL receptor ligand-binding repeat homology <LDLS>
F:3651-3687/Domain: LDL receptor ligand-binding repeat homology <LDLT>
F:3692-3728/Domain: LDL receptor ligand-binding repeat homology <LDLU>
F:3738-3774/Domain: LDL receptor ligand-binding repeat homology <LDLV>
F:3783-3820/Domain: EGF homology <EG14>
F:3826-3858/Domain: EGF homology <EG15>
F:3866-3909/Domain: LDL receptor YWTD-containing repeat homology <YW40>
F:3910-3968/Domain: LDL receptor YWTD-containing repeat homology <YW41>
F:3943-4543/Domain: alpha-2-macroglobulin receptor 85K chain #status predicted <85K>
F:3943-4420/Domain: 85K chain extracellular #status predicted <EXT>
F:3969-4011/Domain: LDL receptor YWTD-containing repeat homology <YW42>
F:4012-4055/Domain: LDL receptor YWTD-containing repeat homology <YW43>
F:4056-4098/Domain: LDL receptor YWTD-containing repeat homology <YW44>
F:4099-4141/Domain: LDL receptor YWTD-containing repeat homology <YW45>
F:4150-4181/Domain: EGF homology <EG16>
F:4199-4230/Domain: EGF homology <EG17>
F:4235-4266/Domain: EGF homology <EG18>
F:4271-4302/Domain: EGF homology <EG19>
F:4307-4338/Domain: EGF homology <EG20>
F:4343-4373/Domain: EGF homology <EG21>
F:4376-4408/Domain: EGF homology <EG22>
F:4421-4443/Domain: transmembrane #status predicted <TMM>
F:4444-4543/Domain: intracellular #status predicted <INT>
F:116,138,187,276,359,448,731,926,1048,1152,1193,1193,1216,1305,1509,1556,1573,1614,1643,
3485,3695,3786,3837,3952,4074,4124,4178,4278/Binding site: carboxylate (Asn) (covalent)
F:168,2995/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
F:2955/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted

Query Match 7.9%; Score 102.5; DB 1; Length 4543;

Best Local Similarity 28.0%; Pred. No. 2.9;

Matches 47; Conservative 12; Mismatches 44; Indels 65; Gaps 14;

QY 5 AMLYGVSMLC--VLDLQPSVVEPCGPGKVGQNGNTRCCSLYAPGKEDCPKERCIC 62

Db 2658 SLCTAPSWVCDGANDCGDYS--DERNC-PG-----GRPKPCANFYA----CPSGRCIP 2704

QY 63 VT-----PEYHCGDPQCKIKHYPCQPGQVRSQGDIVF---GFRCAV---- 102

Db 2705 MTWCTCKEDDCENGEDTHCSERQDKFC--YPVQ-----PECNNHRCISKLWV 2750

QY 103 -----CAMGTFPSAGRDGHCRLWTNCSQFGFLTFPGKTHNAVCIP 144

Db 2751 CDGADDCGDG---SDSDSRCL--TTCSTGSF---QCPG---TYVCVPE 2788

Search completed: October 26, 2005, 15:52:33

Job time : 27.307 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 26, 2005, 15:29:08 ; Search time 112.299 Seconds
(without alignments)
1039.676 Million cell updates/sec

Title: US-09-545-998B-2

Perfect score: 1301

Sequence: 1 MGAWALYGVSMCLVLDLQ.....PEERGEQTEKHLGRWP 228

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 03:*

1: uniprot_prot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	1301	100.0	228	1 TR18_MOUSE	Q35714 mus musculus
2	1294	99.5	250	2 Q8C4K3	Q8C4K3 mus musculus
3	735.5	56.5	241	1 TR18_HUMAN	Q9Y5U5 homo sapien
4	228.5	17.6	255	1 TNR9_HUMAN	Q07011 homo sapien
5	203.5	15.6	256	1 TNR9_MOUSE	P20334 mus musculus
6	184	14.1	211	2 Q8R037	Q8R037 mus musculus
7	175	13.5	276	2 Q9DD2	Q9DD2 gallus gall
8	154	11.8	275	2 Q80W9	Q80W9 mus musculus
9	149.5	11.5	276	2 Q71F55	Q71F55 mus musculus
10	145.5	11.2	196	2 Q8VC17	Q8VC17 mus musculus
11	139	10.7	318	2 Q7T2H3	Q7T2H3 oncorhynch
12	138.5	10.6	270	2 Q75SV8	Q75SV8 felis silve
13	137.5	10.6	290	2 Q76LB4	Q76LB4 paralichthy
14	136	10.5	401	2 Q6P112	Q6P112 mus musculus
15	135.5	10.4	467	2 Q80010	Q80010 gallus gall
16	134	10.3	272	1 TNR4_MOUSE	P47741 mus musculus
17	128	9.8	401	1 T11B_MOUSE	Q08712 mus musculus
18	127.5	9.8	267	2 Q02764	Q02764 oryctolagus
19	127	9.8	278	2 Q8SQ34	Q8SQ34 sus scrofa
20	127	9.8	401	1 T11B_RAT	Q08727 rattus norv
21	126.5	9.7	271	1 TNR4_RAT	P15725 rattus norv
22	125.5	9.6	250	1 TNR7_MOUSE	P41272 mus musculus
23	125	9.6	625	1 TR11_MOUSE	Q35305 mus musculus
24	122	9.4	277	1 TNR4_HUMAN	P43489 homo sapien
25	122	9.4	401	1 T11B_HUMAN	Q00300 homo sapien
26	121.5	9.3	269	1 TNR5_BOVIN	Q28203 bos taurus
27	120.5	9.3	415	1 TNR3_MOUSE	P50284 mus musculus
28	120	9.2	616	1 TR11_HUMAN	Q79666 homo sapien
29	119.5	9.2	274	2 Q7YRL5	Q7YRL5 canis famil
30	119.5	9.2	277	2 Q8WMO2	Q8WMO2 ovis aries
31	119	9.1	1113	1 COR1_MOUSE	Q92319 mus musculus

32	118.5	9.1	277	1 TNR5_HUMAN	P25942 homo sapien
33	118.5	9.1	387	2 Q6GLN3	Q6GLN3 xenopus lae
34	115.5	8.9	223	2 Q86YK5	Q86YK5 homo sapien
35	115.5	8.9	302	2 Q9PUS0	Q9PUS0 salvelinus
36	115	8.8	435	1 TNR3_HUMAN	P36941 homo sapien
37	114	8.8	308	1 ZDH7_HUMAN	Q9NXF8 homo sapien
38	110.5	8.5	300	1 TR6B_HUMAN	Q9S407 homo sapien
39	110.5	8.5	461	2 Q6VAU8	Q6VAU8 rattus norv
40	110.5	8.5	474	1 TR1B_RAT	Q80WY6 rattus norv
41	110.5	8.5	1259	2 Q8K3F9	Q8K3F9 rattus norv
42	108.5	8.3	186	2 Q7ZZY5	Q7ZZY5 gallus gall
43	108	8.3	285	2 Q9W71	Q9W71 oncorhynch
44	107.5	8.3	169	2 Q9JKE0	Q9JKE0 rattus norv
45	107.5	8.3	459	2 Q62327	Q62327 mus musculus

ALIGNMENTS

RESULT 1

ID	TR18_MOUSE	STANDARD;	PRT;	228 AA.
AC	Q35714; Q9JKE1; Q9JKE2; Q9JKE3;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Tumor necrosis factor receptor superfamily member 18 precursor			
DE	(Glucocorticoid-induced TNFR-related protein).			
GN	Name=Tnfrsf18; Synonyms=Gitr;			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
[1]	SEQUENCE FROM N.A. (ISOFORM A).			
RP	STRAIN=C3H;			
RC	MEDLINE=97322352; PubMed=9177197; DOI=10.1073/pnas.94.12.6216;			
RX	Medline=97322352; PubMed=10798444; DOI=10.1089/104454900314474;			
RA	Nocentini G., Giunchi L., Ronchetti S., Krausz L.T., Bartoli A.,			
RA	Moraca R., Migliorati G., Riccardi C.;			
RA	"A new member of the tumor necrosis factor/nerve growth factor			
RT	receptor family inhibits T cell receptor-induced apoptosis."			
RT	Proc. Natl. Acad. Sci. U.S.A. 94:6216-6221(1997).			
[2]	SEQUENCE FROM N.A. (ISOFORM A).			
RP	STRAIN=BALB/c;			
RC	MEDLINE=20256302; PubMed=10798444; DOI=10.1089/104454900314474;			
RX	Nocentini G., Bartoli A., Ronchetti S., Giunchi L., Cupelli A.,			
RA	Delfino D., Migliorati G., Riccardi C.;			
RA	"Gene structure and chromosomal assignment of mouse GITR, a member of			
RT	the tumor necrosis factor/nerve growth factor receptor family."			
RT	DNA Cell Biol. 19:205-217(2000).			
[3]	SEQUENCE FROM N.A. (ISOFORMS B; C AND D).			
RP	TISSUE=Thymus;			
RC	MEDLINE=20292073; PubMed=10836847;			
RX	Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,			
RA	Brunetti L., Migliorati G., Riccardi C.;			
RA	"Identification of three novel mRNA splice variants of GITR."			
RL	Cell Death Differ. 7:408-410(2000).			
[4]	SEQUENCE FROM N.A. (ISOFORM A).			
RP	STRAIN=C57BL/6J; TISSUE=Thymus;			
RC	MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;			
RX	Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,			
RA	Nikado I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,			
RA	Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojibori T.,			
RA	Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,			
RA	Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,			
RA	Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.B., Cousins S.,			
RA	Dalla E., Dragani T.A., Fletcher C.P., Forrest A., Frazer K.S.,			
RA	Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,			
RA	Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis B.D.,			
RA	Kanai A., Kawaji H., Kawasaki Y., Kedzierski R.M., King B.L.,			

RA Kongaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sample C.A., Setou M., Shimada K.,
RA Sulcana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavalan K., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
CC -!- FUNCTION: Receptor for TNFSF18. Seems to be involved in
CC interactions between activated T lymphocytes and endothelial cells
CC and in the regulation of T cell receptor-mediated cell death.
CC Mediated NF-kappa-B activation via the TRAF2/NIK pathway (By
CC similarity).
CC -!- SUBUNIT: Binds to TRAF1, TRAF2, and TRAF3, but not TRAF5 and TRAF6
CC (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoforms A, B and
CC C); secreted (isoform D).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=A;
CC IsoId=O35714-1; Sequence=Displayed;
CC Name=B;
CC IsoId=O35714-2; Sequence=VSP_006510;
CC Name=C;
CC IsoId=O35714-3; Sequence=VSP_006511;
CC Name=D;
CC IsoId=O35714-4; Sequence=VSP_006509;
CC -!- TISSUE SPECIFICITY: Preferentially expressed in activated T
CC lymphocytes.
CC -!- INDUCTION: Up-regulated in peripheral mononuclear cells after
CC antigen stimulation/lymphocyte activation.
CC -!- SIMILARITY: Contains 3 TNFR-Cys repeats.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U82534; AAB91243.1; -;
DR EMBL; AF109216; AAF14231.1; -;
DR EMBL; AF229432; AAF61566.1; -;
DR EMBL; AF229433; AAF61567.1; -;
DR EMBL; AF229434; AAF61568.1; -;
DR EMBL; AK020762; BAC25639.1; -;
DR MGD; MGI:894675; Tnfrsf18.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001368; TNFR_c6.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; FALSE_NEG.
DR PROSITE; PS50050; TNFR_NGFR_2; FALSE_NEG.
KW Alternative splicing; Glycoprotein; Receptor; Repeat; Signal;
KW Transmembrane.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 228 Tumor necrosis factor receptor
FT DOMAIN 20 153 superfamily member 18.
FT TRANSMEM 154 174 Extracellular (Potential).
FT DOMAIN 175 228 Potential.
FT CYTOPLASMIC (Potential).

FT REPEAT 28 61 TNFR-Cys 1.
FT REPEAT 62 101 TNFR-Cys 2.
FT REPEAT 102 142 TNFR-Cys 3.
FT DISULFID 29 44 By similarity.
FT DISULFID 62 74 By similarity.
FT DISULFID 69 82 By similarity.
FT DISULFID 103 122 By similarity.
FT DISULFID 116 141 By similarity.
FT CARBOHYD 36 36 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 40 40 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 121 121 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 134 134 N-linked (GlcNAc...) (Potential).
FT VARSPLIC 121 228 NCSQGFGLTMPPGNKTHNAVCIPEPLTEQYGHLLTVFLWQ
FT AACIFLTVQLGLHIWQLRQHMCPRETQPPFAEVLQSAED
FT ACSFQPEERGEOTEKCHLGRWP -> KDPAIRGGAVV
FT S (in isoform D).
FT /FTid=VSP_006509.
FT ETQPPAEVLQSAEDACSFQPEERGEOTEKCHLGRWP
FT -> VLLQPPSHRRSCQLRLMAASSLRNAGSRQKKSVI
FT WGVGHEAWSSVPOARRIKYTCPLPLVRAGAMLCITLPAW
FT PCSQQQWRKXWYVSGELRLGPMWAAFLI (in isoform
FT B).
FT /FTid=VSP_006510.
FT ETQPPAEVLQSAEDACSFQPEERGEOTEKCHLGRWP
FT -> GOLCPREGENVSQAPHLQPFYRDPAIRGGAVVS (in
FT isoform C).
FT /FTid=VSP_006511.
FT SQ SEQUENCE 228 AA; 25334 MW; 50D8C275D9C56259 CRC64;
Query Match 100.0%; Score 1301; DB 1; Length 228;
Best Local Similarity 100.0%; Pred. No. 5.3e-106; Mismatches 0; Indels 0; Gaps 0;
Matches 228; Conservative 0;
QY 1 MGAWAMLYGVSMCLVLDLGQPSVVEEPCGPGKQVQSGNNTTRCCSLYAPGKEDCPKERC 60
DB 1 MGAWAMLYGVSMCLVLDLGQPSVVEEPCGPGKQVQSGNNTTRCCSLYAPGKEDCPKERC 60
QY 61 ICVTPEYHCGDPQCKICKHYPCQPQQRVESQGDIVFGFRVCACAMGTFSAGRDGHCRLWT 120
DB 61 ICVTPEYHCGDPQCKICKHYPCQPQQRVESQGDIVFGFRVCACAMGTFSAGRDGHCRLWT 120
QY 121 NCSQGFGLTMPPGNKTHNAVCIPEPLTEQYGHLLTVFLWMAACIFFELTVQLGHLHWQL 180
DB 121 NCSQGFGLTMPPGNKTHNAVCIPEPLTEQYGHLLTVFLWMAACIFFELTVQLGHLHWQL 180
QY 181 RQHMCPRETQPPFAEVLQSAEDACSFQPEERGEOTEKCHLGRWP 228
DB 181 RQHMCPRETQPPFAEVLQSAEDACSFQPEERGEOTEKCHLGRWP 228
RESULT 2
Q8C4K3 PRELIMINARY; PRT; 250 AA.
ID Q8C4K3
AC Q8C4K3
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2004 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched
DE library, clone:Cl30084C11 product:tumor necrosis factor receptor
DE superfamily, member 18, full insert sequence.
DE Name=Tnfrsf18;
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RT Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]

RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RA The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitesunai T., Tashiro H., Itoh M.,
RA Sumi N., Iehi Y., Nakamura S., Hazama M., Nishine T., Kashiwagi K.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Ogawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Tanaka T., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takanashi F., Takaku-Akai H., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK081878; BAC38357.1;
DR MGD; MGI:894675; Tnf18.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001368; TNFR_c6.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00208; TNFR; 2.
DR Receptor.
SQ SEQUENCE 250 AA; 27814 MW; 6963E94F4141C16B4 CRC64;
Query Match 99.5%; Score 1294; DB 2; Length 250;
Best Local Similarity 100.0%; Pred. No. 2.4e-105;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGAWMLYGVSMCLVLDLQSPVVEPGCGPKVQNGSGNTRCCSLYAPGKEDCPKRC 60
Db 1 MGAWMLYGVSMCLVLDLQSPVVEPGCGPKVQNGSGNTRCCSLYAPGKEDCPKRC 60
Qy 61 ICVTPEVHCDDPQCKICKHYPCQGRVESQGDIVFGFRVCACAMGTFSGAGDGHCLWT 120

Db 61 ICVTPEVHCDDPQCKICKHYPCQGRVESQGDIVFGFRVCACAMGTFSGAGDGHCLWT 120
Qy 121 NCSQFGFLTMFPGNKTNNVAVCIPELPTQYGLHVIPLVMAACIFFLTTVGLGLHWL 180
Db 121 NCSQFGFLTMFPGNKTNNVAVCIPELPTQYGLHVIPLVMAACIFFLTTVGLGLHWL 180
Qy 181 RQHMCPRETQPPFAEVQLSAEDACSFQPPPEERGRGTQTEKCHLGRW 227
Db 181 RQHMCPRETQPPFAEVQLSAEDACSFQPPPEERGRGTQTEKCHLGRW 227
RESULT 3
TR18 HUMAN
ID TR18 HUMAN STANDARD; PRT; 241 AA.
AC Q9V5U5; O95851; Q9NYJ9;
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 18 precursor
DE (Glucocorticoid-induced TNFR-related protein) (Activation-inducible
DE TNFR family receptor) (UNQ319/PRO364).
GN Name=TNFRSF18; Synonyms=AITR, GITR;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND INTERACTIONS WITH TRAF1; TRAF2 AND
RP TRAF3.
RC TISSUE=Bone marrow;
RX MEDLINE=99175482; PubMed=10074428; DOI=10.1016/S0960-9822(99)80093-1;
RA Gurney A.L., Marsters S.A., Huang R.M., Pitti R.M., Mark D.T.,
RA Baldwin D.T., Gray A.M., Dowd A.D., Brush A.D., Heidens A.D.,
RA Schow A.D., Goddard A.D., Wood W.I., Baker K.P., Godowski P.J.,
RA Ashkenazi A.;
RT "Identification of a new member of the tumor necrosis factor family
RT and its receptor, a human ortholog of mouse GITR.";
RL Curr. Biol. 9:215-218(1999).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=T-cell;
RX MEDLINE=99156876; PubMed=10037686; DOI=10.1074/jbc.274.10.6056;
RA Kwon B., Yu K.-Y., Ni J., Yu G.-L., Jang I.-K., Kim Y.-J., Xing L.,
RA Liu D., Wang S.-X., Kwon B.S.;
RT "Identification of a novel activation-inducible protein of the tumor
RT necrosis factor receptor superfamily and its ligand.";
RL J. Biol. Chem. 274:6056-6061(1999).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Thymus;
RX MEDLINE=20292073; PubMed=10836847;
RA Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,
RA Brunetti L., Migliorati G., Riccardi C.;
RT "Identification of three novel mRNA splice variants of GITR.";
RL Cell Death Differ. 7:408-410(2000).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Baton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heidens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wleand D., Woods K., Xie M.-H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P., Gray A.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
RN [5]
RP SEQUENCE OF 26-40.

RN [6] SEQUENCE FROM N.A.
 RA Pearce A.;
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 RP [7]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Kidney;
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Heiton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [8]
 RP SEQUENCE OF 24-38.
 RX PubMed=15340161; DOI=10.1110/ps.04682504;
 RA Zhang Z., Henzel W.J.;
 RT "Signal peptide prediction based on analysis of experimentally
 verified cleavage sites.";
 RL Protein Sci. 13:2819-2824(2004).
 RN [9]
 RP INTERACTIONS WITH TRAF1; TRAF2 AND TRAF3.
 RX MEDLINE=98078711; PubMed=9418902;
 RA Arch R.H., Thompson C.B.;
 RT "4-1BB and Oxa40 are members of a tumor necrosis factor (TNF)-nerve
 growth factor receptor subfamily that bind TNF receptor-associated
 factors and activate nuclear factor kappaB.";
 RL Mol. Cell. Biol. 18:558-565(1998).
 RN [10]
 RP INTERACTIONS WITH TRAF1 AND TRAF2.
 RX MEDLINE=98270914; PubMed=9607925;
 RA Saouli K., Lee S.Y., Cannons J.L., Yeh W.C., Santana A.,
 RA Goldstein M.D., Bangia N., DeBenedette M.A., Mak T.W., Choi Y.,
 RA Watts T.H.;
 RT "CD28-independent, TRAF2-dependent costimulation of resting T cells by
 4-1BB ligand.";
 RL J. Exp. Med. 187:1849-1862(1998).
 RN [11]
 RP INTERACTION WITH LRR-REPEAT PROTEIN 1/LRR-1.
 RX MEDLINE=21662677; PubMed=11804328; Hill J.M., Kim J.-D., Kwon B.S.;
 RA Jang I.-K., Lee Z.-H., Kim H.-H., Hill J.M., Kim J.-D., Kwon B.S.;
 RT "A novel leucine-rich repeat protein (LRR-1): potential involvement in
 4-1BB-mediated signal transduction.";
 RL Mol. Cells 12:304-312(2001).
 CC -1- FUNCTION: Receptor for TNFSF14/4-1BBL. Possibly active during T
 cell activation.
 CC -1- SUBUNIT: Interacts with TRAF1, TRAF2 and TRAF3. Interacts with
 LRR-repeat protein 1/LRR-1.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Expressed on the surface of activated T cells.
 CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
 CC -1- DATABASE: NAME=PROW; NOTE=CD guide CDw137 entry;
 WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cdw137.htm".
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U03397; AAA53133.1; -;
 DR EMBL; L12964; AAA62478.2; -;
 DR EMBL; AY438976; AAR05440.1; -;
 DR EMBL; AL009183; CAB57398.1; -;
 DR EMBL; BC006196; AAH06196.1; -;
 DR FIR; I38426; I38426.
 DR HSSP; Q92956; LJMA.
 DR H-InvDB; HIX0000096; -;
 DR MIM; 602250; -;
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0004872; F:receptor activity; TAS.
 DR GO; GO:0004973; P:induction of apoptosis; TAS.
 DR GO; GO:0008285; P:negative regulation of cell proliferation; TAS.
 DR InterPro; IPR001368; TNFR_c6.
 DR Pfam; PF00020; TNFR_c6; 2.
 DR SMART; SM00208; TNFR_2.
 DR PROSITE; PS00652; TNFR_NGFR_1; 1.
 DR PROSITE; PS00500; TNFR_NGFR_2; 1.
 KW Direct protein sequencing; Glycoprotein; Polymorphism; Receptor;
 KW Repeat; Signal; Transmembrane.
 FT SIGNAL 1 23
 FT CHAIN 24 255
 FT DOMAIN 24 186
 FT TRANSMEM 187 213
 FT DOMAIN 214 255
 FT REPEAT 24 45
 FT REPEAT 47 86
 FT REPEAT 87 118
 FT REPEAT 119 159
 FT REPEAT 214 255
 FT DISULFID 28 37
 FT DISULFID 31 45
 FT DISULFID 48 62
 FT DISULFID 65 78
 FT DISULFID 68 86
 FT DISULFID 88 94
 FT DISULFID 99 106
 FT DISULFID 102 117
 FT DISULFID 121 133
 FT DISULFID 139 158
 FT CARBOHYD 138 138
 FT CARBOHYD 149 149
 FT VARIANT 56 56
 FT VARIANT 115 115
 FT VARIANT 176 176
 FT SEQUENCE 255 AA; 27899 MW; F3A563FE5F00460 CRC64;
 Query Match 17.6%; Score 228.5; DB 1; Length 255;
 Best Local Similarity 27.2%; Pred. No. 5.2e-12;
 Matches 68; Conservative 30; Mismatches 97; Indels 55; Gaps 10;
 QY 11 SMLCVLDLQGPSVVEEP-----CCGPGKVQVNGSNNT-----RCCS 46
 DB 11 TLLVLNFERLSLQDPCSNCPAGTFCDNNRNQICSPCPNPSFSSAGGQRTCDICRCKG 70
 QY 47 LYAPGKE--DCPKERCICVTPEYHCGPQCKICKHYCQPCQVSGDIVFGRCVACA 104
 DB 71 VFTRKECSSTNAECDC-TFGFHLGAGCSMCSEQ-DCQGGQLTKKG-----CKDCC 121
 QY 105 MGFESAGRGDCHRLWNCSTQFGFLTFPGNKNTHAVCIPE-----PLPTQY 151
 DB 122 FGTNDQKRGICRPWTNCSLDGKSVLVNGTKERDVCGSPADLSPGNASSVTPAPAREP 181
 QY 152 GHLTVIF-----LVMAACIFPLTTVLGLHLIWLRRQHMCPRETQPFAB-VOLS-AEDAC 204

```

Db 182 GSPQIISFFALTALLFLFLRFSVVKRKKLLYIFKQPFMRPVQTOEDGC 241
Qy 205 SQFPPEERG 214
Db 242 SCRFPEERG 251

RESULT 5
TNR9_MOUSE
ID TNR9_MOUSE STANDARD; PRT; 256 AA.
AC P20334;
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 9 precursor (4-1BB
DE ligand receptor) (T-cell antigen 4-1BB) (CD137 antigen).
GN Name=Tnfrsf9; Synonyms=Cd137, Cd157, ILA, Ly63;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RX MEDLINE=89184547; PubMed=2784565;
RA Kwon B.S., Weissman S.M.;
RT "cDNA sequences of two inducible T-cell genes."
RL Proc. Natl. Acad. Sci. U.S.A. 86:1963-1967(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=94179805; PubMed=8133039;
RA Kwon B.S., Kozak C.A., Kim K.K., Pickard R.T.;
RT "Genomic organization and chromosomal localization of the T-cell
RT antigen 4-1BB."
RL J. Immunol. 152:2256-2262(1994).
RN [3]
RP CHARACTERIZATION, AND SEQUENCE OF 24-29.
RX MEDLINE=93139510; PubMed=7678621;
RA Pollok K.E., Kim Y.-J., Zhou Z., Hurtado J., Kin K.K., Pickard R.T.,
RA Kwon B.S.;
RT Inducible T cell antigen 4-1BB. Analysis of expression and
RT function."
RL J. Immunol. 150:771-781(1993).
CC -!- FUNCTION: Receptor for TNFSF14/4-1BBL. Possibly active during T
CC cell activation.
CC -!- SUBUNIT: Principally an homodimer, but also found as a monomer.
CC Associates with p56-LCK. Interacts with TRAF1, TRAF2 and TRAF3 (by
CC similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed on the surface of activated T cells.
CC -!- INDUCTION: Optimal by PMA and ionomycin.
CC -!- SIMILARITY: Contains 4 TNER-Cys repeats.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; J04492; AAA0167.1; -.
CC EMBL; U02567; AAA93113.1; -.
CC PIR; B32393; B32393.
CC FDB; ID00; X-ray; G/H/I/J/K-230-236.
CC MGD; MGI:1101059; Tnfrsf9.
CC InterPro; IPR009030; Grow_fac_recept.
CC InterPro; IPR001368; TNFR c6.
CC Pfam; PF00020; TNFR c6; 1.
CC SMART; SM00208; TNFR; 2.
CC PROSITE; PS00652; TNFR_NGFR_1; 1.
CC PROSITE; PS50050; TNFR_NGFR_2; FALSE_NEG.

```

```

KW 3D-structure; Direct protein sequencing; Glycoprotein; Receptor;
KW Repeat; Signal; Transmembrane.
FT SIGNAL 1 23
FT CHAIN 24 256
FT Tumor necrosis factor receptor
FT superfamily member 9.
FT Extracellular (Potential).
FT Potential.
FT Cytoplasmic (Potential).
FT TNFR-Cys 1.
FT TNFR-Cys 2.
FT TNFR-Cys 3.
FT TNFR-Cys 4.
FT By similarity.
FT DISULFID 28 37
FT DISULFID 31 44
FT DISULFID 47 61
FT DISULFID 64 77
FT DISULFID 67 85
FT DISULFID 87 93
FT DISULFID 98 105
FT DISULFID 101 116
FT DISULFID 119 133
FT DISULFID 139 158
FT CARBOHYD 128 128
FT CARBOHYD 138 138
FT SEQUENCE 256 AA; 27598 MW; 93A10D03C60813C4 CRC64;
SQ SEQUENCE 256 AA; 27598 MW; 93A10D03C60813C4 CRC64;

Query Match 15.6%; Score 203.5; DB 1; Length 256;
Best Local Similarity 29.8%; Pred. No. 8.1e-10;
Matches 64; Conservative 26; Mismatches 84; Indels 41; Gaps 10;

Qy 22 SVVEPGCGKVGKQNGSNTRCCSLYAPGKEDCP---KERCICVTPEVHCGDPOCKICK 78
Db 54 SIGGGPNC-----NIRCVAGYFRFXKFCSTHNAECEI-EGFHCIGPQTRCE 102
Qy 79 HVPQPGQVESQGDIVFGRCVACAMGTFSS-AGRDGHCRLWTNGSQGFITMFPQNKTH 137
Db 103 K-DCRPGQELTKG-----CKTCSLGTENDQNGTVCPRPWNCSLDGRSVLKTGTTEK 154
Qy 138 NAVCIP-----EPLPTEQY-----GH-----LTVFILVMAACIFLTTVQGLHIWQLR 181
Db 155 DWVCGPPVVSFSPSTTISVTPEGGPGHSLQVLTLFLALTSALLALIFITLLFSVLKWI 214
Qy 182 RQHMCPRETQPPAEVOLSA--EDACSFQFPPEERG 214
Db 215 RKKPFPHFQPKFKTKTTGAQAEDACSCRCPOEEG 249

RESULT 6
QBR037 ID QBR037 PRELIMINARY; PRT; 211 AA.
AC QBR037;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Tnfrsf9 protein.
GN Name=Tnfrsf9;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RX TISSUE=Uterus;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

```



```

Db 94 GTQEECLPWNCSAFO-QEVRGRTNSTDTTCSSQ-----VVYYVW-SILLPLVI 140
Qy 171 VOGLHWHQL-RQHM-----CPRETQPPAEVQLSAEDACSFQPEEERG-EQTEEK 220
Db 141 VGVGIAGLICTRRHLSVVAKELEFPQOEQ-----QENTIRFPVTEVGFATTEE 192

RESULT 11
Q7T2H3
ID Q7T2H3 PRELIMINARY; PRT; 318 AA.
AC Q7T2H3;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Tumour necrosis factor receptor.
GN Name=tnfr;
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
SEQUENCE FROM N.A.
RP TISSUE=Head kidney;
RA Zou J., Secombes C.J.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ517804; CAD57165.1; -.
DR HSSP; Q92956; 1JMA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001368; TNFR_c6.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF000208; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
DR PROSITE; PS50050; TNFR_NGFR_2; 4.
KW Receptor.
SQ SEQUENCE 318 AA; 35254 MW; 78F8135011283B43 CRC64;

Query Match 10.7%; Score 139; DB 2; Length 318;
Best Local Similarity 23.7%; Pred. No. 0.00045;
Matches 50; Conservative 28; Mismatches 91; Indels 42; Gaps 9;

Qy 29 CGFGKVGSGNN--TRCCSLYAPGKDCPKERCICVTPEYHCGDPOCKICKHP-CQPG 85
Db 61 CLPCRVYSSNQKVLREC-----EASSDRQCVCKT-GYYCTDDGCEHCLPVTLCPLG 112
Qy 86 QRVESQDIVFGFRVCACAMGTFSGRDG--HCLRLWNCQSQFGFLTFMFGNKNTHNVC-- 141
Db 113 SGVYNQANPQNDTVCAPCQPGTGNFNDFTHCQSHTRCGDLGKEVKSAGTETTDVCGA 172
Qy 142 ----IPLEPLTEQVGHLLTVI-FLVMAACIFFLTVQLGLHIWQLRQHMCPRET----- 190
Db 173 FISRWHLTSLWAGLVVTSLLIILICIV-----WRAKQSYNPANSSSPGIP 221
Qy 191 -----QFAEVQLSAEDACSFQPEEERGQ 216
Db 222 VEPAPSSFAPEALKFPTECNHWSLDQKATE 252

RESULT 12
Q75SV8
ID Q75SV8 PRELIMINARY; PRT; 270 AA.
AC Q75SV8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE CD134 homologue.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]

```

```

RP SEQUENCE FROM N.A.
RA Shimajima M., Miyazawa T., Ikeda Y., McMonagle E.L., Haining H.,
RA Akashi H., Takeuchi Y., Hosie M.J., Willett B.J.;
RT "Use of CD134 as a primary receptor by the feline immunodeficiency
RT virus.";
RL Science 0:0-0(2004).
DR EMBL; AB128982; BAD11363.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
SQ SEQUENCE 270 AA; 28731 MW; 36A40BAD261140D1 CRC64;

Query Match 10.6%; Score 138.5; DB 2; Length 270;
Best Local Similarity 26.3%; Pred. No. 0.00042;
Matches 59; Conservative 18; Mismatches 72; Indels 75; Gaps 12;

Qy 29 CGFGKVGSGNNTRC-----CSLYAPG-----KEDC-----PKERC 61
Db 47 CFP-----GYGMESRCSGDQDTKCLQCSGFYNEAVNYPCKPCTCQNRSGSEPKQRC- 100
Qy 62 CVTPEYHCGDPOCKICKHPYCPQQRVESQGDIVFGFRVCACAMGTFSGRDGCHRLWNTN 121
Db 101 --TP-----TQDTVCR---CRPG--TEPDQGYDRGVDCAPCPPPGHFSPGDDQACKPWTN 147
Qy 122 CSQFGLTFMFGNKNTHNVCIPPEPLTEQVGHLLTVFLVMAACIFFLTVQLGLHIWQLR 181
Db 148 CTLAGKRTLRLPASQSGSDAVCEDRSPPA-----TTP-----WETQ 181
Qy 182 RQHMCPRTPQFAEVQLSAEDACSFQFP--EEREGEOTEKCHLG 224
Db 182 GPVPRPTTQPTTAWPRTSQE--PFTTPAEPPPGQLAAVLIG 223

RESULT 13
Q76LB4
ID Q76LB4 PRELIMINARY; PRT; 290 AA.
AC Q76LB4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE CD40.
GN Name=CD40;
OS Paralicthys olivaceus (Japanese flounder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronectoidae; Paralicthidae; Paralicthys.
OX NCBI_TaxID=8255;
RN [1]
RP SEQUENCE FROM N.A.
RA Park C., Hirono I., Aoki T.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Park C., Hirono I., Aoki T.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB081752; BAC87848.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR006209; EGF_Like.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
SQ SEQUENCE 290 AA; 32396 MW; B6FCF9E35305DFAA CRC64;

Query Match 10.6%; Score 137.5; DB 2; Length 290;
Best Local Similarity 22.9%; Pred. No. 0.00056;
Matches 46; Conservative 28; Mismatches 74; Indels 53; Gaps 11;

Qy 26 EPGCGPGKVQNGSGNTRCCSLYAPGKDCPKERCICVTPEYHCGDPOCKIC-KHYPCQP 84

```

```
Db 78 QYCDPNK-----NLRVTKPESKTKQ-----SPICILL-GFHCSSGTCVTCVPHATCKP 125
QY 85 GQVRSQGDIVFGFRCAACAMGTFAGR--DGHCLRWNCNSQGFGLTMFPNGKTHNAVCI 142
Db 126 GQWAKIKGNLTHDTCVSCSPESFSTSHSWSSVCTKWTEC-BSGYHIQESGTNESDNLCV 184
QY 143 PEPLPTEQYGHVTVIFLWNAACIFLTVQ-IGLHIMQLRRQHMCPRETQPPAEVQLSAE 201
Db 185 E---PFRHHGGL-----IACVAVGSLAVVGLMVC-----LCKGET----- 217
QY 202 DACSQFPPEEREGEOTEKCH 222
Db 218 -----KORAKDYLESCH 229

RESULT 14
Q6P112 PRELIMINARY; PRT; 401 AA.
AC Q6P112;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Tumor necrosis factor receptor superfamily, member 11b
DE (Osteoprotegerin).
GN Name=TnfRsf11b;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Limb;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.W., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Limb;
RA Strausberg R.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC049782; AH49782.1; -.
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IDA.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0042489; P:negative regulation of ontogenesis (sensu. .; IDA.
DR InterPro; IPR000488; Death.
DR InterPro; IPR011029; DEATH like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00017; DEATH DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
KW Receptor.
```

```
SQ SEQUENCE 401 AA; 45965 MW; 7C708B52EB46BA0E CRC64;
Query Match 10.5%; Score 136; DB 2; Length 401;
Best Local Similarity 28.2%; Pred. No. 0.001;
Matches 44; Conservative 10; Mismatches 54; Indels 48; Gaps 7;
QY 45 CSLVAPG---KEDCP-KERCICV-----TPEVHCGD-----PQCK----- 75
Db 41 CDKCAPGYLKQHCCTVRRKTLCLVPCPDHSYTDSTWHTSDCVCSVPVKELQSVKQECNRT 100
QY 76 ---IC-----KHVPQGPQGVRSQGDIVFGFRCAACAMGTFSS--AGRDGHC 116
Db 101 HNRVCECEEGRYLEIFCLKHSRSCPPGSGVQAGTPEQNTVCKKCPDGFSGSETSSKAPC 160
QY 117 RLWNCNSQGFGLTMFPNGKTHNAVCIPEPLTEQYQ 152
Db 161 RKHTNCSTFGLLLIQKGNATHDNCVSGNREATQKCG 196

RESULT 15
Q80010 PRELIMINARY; PRT; 467 AA.
ID Q80010;
AC Q80010;
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE CD30 protein precursor.
GN Name=CD30;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15356338;
RA Burgess S.C., Young J.R., Baaten B.J.G., Hunt L., Ross L.N.J.,
RA Parcells M.S., Kumar M.S., Tregaskes C.A., Lee L.F., Davison T.F.;
RT "Marek's disease is a natural model for lymphomas overexpressing
RT Hodgkin's disease antigen (CD30).";
RL Proc. Natl. Acad. Sci. U.S.A. 101:13879-13884(2004).
[2]
RP SEQUENCE FROM N.A.
RA Burgess S.C.;
RL Thesis (1998); Bristol University, UK.
DR EMBL; AJ276964; CAC79223.1; -.
DR HSSP; Q92956; 1JWA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005031; F:tumor necrosis factor receptor activity; IEA.
DR GO; GO:0019221; P:cytokine and chemokine mediated signaling p. .; IEA.
DR InterPro; IPR011366; TNFprecept_2.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 1.
DR PIRSF; PIRSF001968; TNFR_2; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
KW Signal.
FT SIGNAL.
FT CHAIN 1 21 Potential.
FT CHAIN 22 467 CD30 protein.
SQ SEQUENCE 467 AA; 51350 MW; F9AD4F7DEEC8588 CRC64;
Query Match 10.4%; Score 135.5; DB 2; Length 467;
Best Local Similarity 21.1%; Pred. No. 0.0013;
Matches 71; Conservative 33; Mismatches 95; Indels 137; Gaps 18;
QY 1 MGAWMLYGVSMCLVLDLQSPSVVEEPGCGPKGVONGSGNWT--RCC-----SLYAPCK-- 52
Db 8 LGLWLLLL---LQDTQGAQPQPPFTSSHSC--DTLKNWFYDTLGRCCYQCPSPGYAKKSC 62
QY 53 -----EDC-----PKERC-ICV--TPEYH-----CGDPQCKIC----- 77
```

```

Db 63 PMDPDEDCMRGPEQYLNSPFRCDACVLCTKEPLVEKAPCSFNSSRVCSRCRPGMFCQ 122
QY 78 -----KHYPGQPGORVESQGDIVGFRFCVACAMGTFS--AGRDGHCRLLWTNCSQ 124
Db 123 TAAKNTCMRCORHTACKPGFGVKIRGTSETDVSCECPFGTFSDQSSSTDVCKPHTDCAK 182
QY 125 FGFLTMFPNGKTHNAYC-----141
Db 183 LNKVAGKGNATHDQVCTDQLPSYLTPTDTSSIRITNETDDSDVLKENANPVTLASILSSA 242
QY 142 ---IPEPLPTEQ-----YGHLTVIFLVMAACIFELTTVOLG-LHIWQLRROHMCP 187
Db 243 TTEIPGSTPEEALAGTSPTLAKGETTTTGLVFWAVVLSVMVLPVGMLSFWQWK---VCK 299
QY 188 RE-----TQPPFAEVOLSAEDACSFQPEEE 212
Db 300 KRIFILKQKRSDLVDKYAKITLTT-DKC-----PEEE 330

```

Search completed: October 26, 2005, 15:51:38
 Job time : 118.299 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 26, 2005, 15:28:42 ; Search time 141.311 Seconds
(without alignments)
659.602 Million cell updates/sec

Title: US-09-545-998B-4
Perfect score: 1386
Sequence: 1 MAQHGAMGAFALCGLALIC.....EEBGRSAAEKRLGLLWV 241

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_16Dec04:*

- 1: geneseqp1980s:*
- 2: geneseqp1980s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1386	100.0	241	2 AAW37839	Aaw37839 Amino aci
2	1386	100.0	241	2 AAY06605	Aay06605 Human TNF
3	1386	100.0	241	3 AAB33431	Aab33431 Human PRO
4	1386	100.0	241	3 AAY71467	Aay71467 Human PRO
5	1386	100.0	241	3 AAB27651	Aab27651 Human pro
6	1386	100.0	241	3 AAY95895	Aay95895 Human tum
7	1386	100.0	241	3 AAB24409	Aab24409 Human PRO
8	1386	100.0	241	4 AAB47054	Aab47054 Human PRO
9	1386	100.0	241	4 AAB20115	Aab20115 Human imm
10	1386	100.0	241	4 AAB53090	Aab53090 Human ang
11	1386	100.0	241	4 AAB47289	Aab47289 PRO364 po
12	1386	100.0	241	4 AAB50982	Aab50982 Human PRO
13	1386	100.0	241	4 AAB50910	Aab50910 Human PRO
14	1386	100.0	241	5 AAE28161	Aae28161 Human TRI
15	1386	100.0	241	6 AAB08442	Aab08442 Amino aci
16	1386	100.0	241	6 AAO16574	Aao16574 Human tum
17	1386	100.0	241	6 AAO23091	Aao23091 Human ene
18	1386	100.0	241	7 ADN39966	Adn39966 Cancer/an
19	1386	100.0	241	8 ADH43131	Adh43131 Human TNF
20	1386	100.0	241	8 ADL91869	Adl91869 Human PRO
21	1386	100.0	241	8 ADO20289	Ado20289 Human PRO
22	1386	100.0	241	8 ADP55559	Adp55559 Human PRO
23	1386	100.0	241	8 ADT94287	Adt94287 Human PRO
24	1382	99.7	240	8 ADR46662	Adr46662 Cancer-as
25	1347	97.2	235	3 AAY44825	Aay44825 Human mol

ALIGNMENTS

RESULT 1

AAW37839

ID AAW37839 standard; protein; 241 AA.

XX AC AAW37839;

XX DT 28-JUL-1998 (first entry)

XX DE Amino acid sequence of the human 312C2 T cell protein.

XX KW Human 312C2 T cell protein; thymus cell; spleen cell; T cell;
 KW antigen-specific T cell proliferation; cytokine production by T-cell;
 KW apoptosis; cancer; haematopoietic cells; lymphoid cell;
 KW autoimmune disorders.

XX OS Homo sapiens.

XX PN WO9806842-A1.

XX PD 19-FEB-1998.

XX PF 14-AUG-1997; 97WO-US013931.

XX PR 16-AUG-1996; 96US-00689943.

XX PA 07-OCT-1996; 96US-0027901P.

XX PI (SCHE) SCHERING CORP.

XX PI Gorman DM, Randall TD, Zlotnik A;

XX DR WPI; 1998-159534/14.

XX DR N-PSDB; AAV19153.

XX FT Isolated 312C2 T cell gene - used to develop products for treating, e.g.
 cancers, auto-immune disorders, transplantation rejection and other T
 cell disorders.

XX PS Claim 2; Page 59-60; 71pp; English.

XX CC This is the amino acid sequence encoding the human 312C2 T cell protein.
 CC The 312C2 proteins are expressed in thymus cells and are induced on T
 CC cells and spleen cells following activation. Engagement of 312C2
 CC stimulates proliferation of T cell clones, antigen-specific proliferation
 CC and cytokine production by T-cells, and potentiates T cell expansion or
 CC apoptosis. The products can be used in the treatment of conditions
 CC associated with abnormal physiology or development, including abnormal
 CC proliferation, e.g. cancerous conditions or degenerative conditions. They
 CC can be used in the regulation or development of haematopoietic cells,

[illegible]

PT	responses.
XX	Claim 17; Fig 2A; 104pp; English.
XX	The present sequence represents human PRO364, a novel member of the
CC	tumour necrosis factor receptor family. The sequence was deduced from a
CC	bone marrow cDNA clone (see AAX87670). Methods for the recombinant
CC	production of PRO364 polypeptides, e.g. in CHO, Escherichia coli or yeast
CC	host cells, are provided. Claimed polypeptides comprise amino acids 1-
CC	241, 1-X, 26-241 (i.e. the mature protein) and 26-X of the present
CC	sequence, where X is any one of amino acid residues 157-167 of PRO364.
CC	PRO364 polypeptides are useful for modulating apoptosis, NF-KB activation
CC	and proinflammatory or autoimmune responses in mammalian cells (claimed).
CC	Chimeric molecules comprising a PRO364 polypeptide fused to a
CC	heterologous sequence such as epitope tag or immunoglobulin Fc region are
CC	also claimed. PRO364 can be used in assays to identify other proteins or
CC	molecules involved in binding interactions. This is useful for
CC	identifying inhibitors or agonists of receptor/ligand binding. The PRO364
CC	polypeptides may also be combined with an agent that is cytotoxic, e.g.
CC	chemotherapeutic or a growth inhibitor. PRO364 antibodies are useful in
CC	diagnostic methods, purification methods and also in therapy, e.g. as
CC	inhibitors
XX	
XX	Sequence 241 AA;
QY	Query Match 100.0%; Score 1386; DB 2; Length 241;
DB	Best Local Similarity 100.0%; Pred. NO. 2.2e-101;
DB	Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY	1 MAQHGANGAFRALCGALLCALSGORPTGCGPGCGRLILGTGTDCRCRVHTRCCRD 60
DB	1 MAQHGANGAFRALCGALLCALSGORPTGCGPGCGRLILGTGTDCRCRVHTRCCRD 60
QY	61 YPEECCSEWDCMCVQPEFHCGBPCCCTTCRHHPCPGQGVQSGKFSFGFQICDCASTGF 120
DB	61 YPEECCSEWDCMCVQPEFHCGBPCCCTTCRHHPCPGQGVQSGKFSFGFQICDCASTGF 120
QY	121 SGGHEGHCKPWTDTCTQGFGLTVFPGNKTHNAVCPGSPAPPLGWLTVLLAAVACVLLL 180
DB	121 SGGHEGHCKPWTDTCTQGFGLTVFPGNKTHNAVCPGSPAPPLGWLTVLLAAVACVLLL 180
QY	181 TSAQLGLHIWQLRSQCMWPRETOLLLLEVPSTEDARSCQPFEEBGRGSAEKGRLGDLW 240
DB	181 TSAQLGLHIWQLRSQCMWPRETOLLLLEVPSTEDARSCQPFEEBGRGSAEKGRLGDLW 240
QY	241 V 241
DB	241 V 241
RESULT 3	
AAB33431	
ID	AAB33431 standard; protein; 241 AA.
XX	
XX	AAB33431;
XX	
DT	29-JAN-2001 (first entry)
DE	Human PRO364 protein UNQ319 SEQ ID NO:92.
XX	
XX	Human; immune related disease; diagnosis; antinflammatory; cardiac;
KW	dermatologic; antiarthritic; antirheumatic; immunosuppressive;
KW	haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;
KW	antianaemic; hepatotropic; virucide; antipneumonia; antiallergic;
KW	antistomatitis; systemic lupus erythematosus; rheumatoid arthritis;
KW	osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;
KW	idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
KW	systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
KW	autoimmune thrombocytopenia; immune-mediated renal disease;
KW	demyelinating disease; hepatobiliary disease; Whipple's disease;
KW	inflammatory bowel disease; gluten-sensitive enteropathy;
KW	autoimmune disease; immune-mediated skin disease; allergic disease;
KW	immunologic disease; transplantation associated disease;

graft rejection; graft-versus-host-disease.

Homo sapiens.

WO200053758-A2.

14-SEP-2000.

02-MAR-2000; 2000WO-US005841.

08-MAR-1999; 99WO-US005028.

10-MAR-1999; 99US-0123618P.

12-MAR-1999; 99US-0123957P.

23-MAR-1999; 99US-0125775P.

12-APR-1999; 99US-0128849P.

20-APR-1999; 99WO-US0008615.

28-APR-1999; 99US-0131445P.

04-MAY-1999; 99US-0132371P.

14-MAY-1999; 99US-0134287P.

02-JUN-1999; 99WO-US012252.

23-JUN-1999; 99US-0141037P.

20-JUL-1999; 99US-0144758P.

26-JUL-1999; 99US-0145698P.

28-JUL-1999; 99US-0146222P.

01-SEP-1999; 99WO-US020111.

08-SEP-1999; 99WO-US020594.

13-SEP-1999; 99WO-US020944.

15-SEP-1999; 99WO-US021090.

15-SEP-1999; 99WO-US021547.

05-OCT-1999; 99WO-US023089.

29-OCT-1999; 99US-0162506P.

28-NOV-1999; 99WO-US028214.

30-NOV-1999; 99WO-US028313.

30-NOV-1999; 99WO-US028409.

01-DEC-1999; 99WO-US028301.

01-DEC-1999; 99WO-US028634.

02-DEC-1999; 99WO-US028551.

02-DEC-1999; 99WO-US028564.

02-DEC-1999; 99WO-US028565.

16-DEC-1999; 99WO-US030095.

20-DEC-1999; 99WO-US030999.

30-DEC-1999; 99WO-US031274.

05-JAN-2000; 2000WO-US000219.

06-JAN-2000; 2000WO-US000277.

06-JAN-2000; 2000WO-US000376.

11-FEB-2000; 2000WO-US003565.

Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus.

Claim 33; Fig 36; 309pp; English.

The present invention describes sixty four human PRO proteins which can be used in the treatment of immune related diseases. The human PRO proteins, anti-PRO antibodies, agonists and antagonists are useful for treating and diagnosing immune related disorders. The disorders are selected from systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic

anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central and peripheral nervous systems, hepatobiliary diseases, inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune or immune-mediated skin diseases, allergic diseases, immunological diseases of the lung, and transplantation associated diseases including graft rejection and graft-versus-host-disease. AAC58397 to AAC58578 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB33477 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention

XX Sequence 241 AA;

Query Match 100.0%; Score 1386; DB 3; Length 241;
Best Local Similarity 100.0%; Pred. No. 2.2e-101;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHGAMGAFRALCGLALCALSLGQRTGGPGCGPGRLLLTGTDDARCRVHTTRCCRD 60
|||
Db 1 MAQHGAMGAFRALCGLALCALSLGQRTGGPGCGPGRLLLTGTDDARCRVHTTRCCRD 60
|||

QY 61 YFGECCSEWDCMCVQPFHCDDPCCTTCRHHPCPGQVQSGKFSFGQCIDCASGTF 120
|||
Db 61 YFGECCSEWDCMCVQPFHCDDPCCTTCRHHPCPGQVQSGKFSFGQCIDCASGTF 120
|||

QY 121 SGHGEGCHKPWTDTQFGFLTVFPGNKTHNAVCPGSPPAEPLGMLTVLLVAACVLLL 180
|||
Db 121 SGHGEGCHKPWTDTQFGFLTVFPGNKTHNAVCPGSPPAEPLGMLTVLLVAACVLLL 180
|||

QY 181 TSAQLGLHIWQLRSQCMWPRETQLLLEVPSPSTDARSQFPPEBERGERSAEKRGRLDLW 240
|||
Db 181 TSAQLGLHIWQLRSQCMWPRETQLLLEVPSPSTDARSQFPPEBERGERSAEKRGRLDLW 240
|||

QY 241 V 241

Db 241 V 241

RESULT 4

AA71467
ID AA71467 standard; protein; 241 AA.

XX AA71467;

XX AC (first entry)

XX 08-NOV-2000 (first entry)

XX Human PRO364 protein.

XX PRO364; DNA47365-1206; human; ATCC No: 209436; antiproliferative;
neoplastic cell growth inhibitor; cytostatic; treatment; cancer; tumour;
breast; prostate; colon; lung; renal; ovarian; central nervous system;
CNS; leukemia; melanoma; Expressed Sequence Tag; EST; TNFR homologue;
tumour necrosis factor receptor; GTR protein homologue.

XX Homo sapiens.

Key	Location/Qualifiers
Peptide	1..25
/label= Signal_peptide	
Modified-site	5..11
/note= "N-myristoylation site"	
Modified-site	8..14
/note= "N-myristoylation site"	
Modified-site	25..31
/note= "N-myristoylation site"	
Protein	26..241
/label= Mature_PRO364_protein	
Modified-site	30..36
/note= "N-myristoylation site"	
Modified-site	33..39
/note= "N-myristoylation site"	
Modified-site	118..124

FT FT Modified-site /note= "N-myristoylation site"
122. .128
FT FT Modified-site /note= "N-myristoylation site"
146. .150
FT FT Modified-site /note= "Asn is N-glycosylated"
156. .162
FT FT Modified-site /note= "N-myristoylation site"
163. .183
FT FT Domain /label= Transmembrane_domain
166. .177
FT FT Binding-site /note= "Prokaryotic membrane lipoprotein lipid attachment
site"
171. .193
FT FT Region /note= "Leucine zipper pattern"
XX XX WO200032778-A2.
XX XX 08-JUN-2000.
XX XX 30-NOV-1999; 99WO-US028409.
XX XX 01-DEC-1998; 98WO-US025108.
XX XX 16-DEC-1998; 98US-0112850P.
XX XX 22-DEC-1998; 98US-0113296P.
XX XX 20-JUL-1999; 99US-0144758P.
XX XX 26-JUL-1999; 99US-0145698P.
XX XX (GETH) GENENTECH INC.
XX XX Chen J, Goddard A, Gurney AL, Hillan K, Napier M, Wood WI;
XX XX WPI; 2000-412325/35.
XX XX N-PSDB; AAD01240.
XX XX New composition useful for inhibiting neoplastic cell growth and for
XX XX treating cancers, comprises PRO655, PRO344 or PRO364 polypeptide or their
XX XX antagonists.
XX XX Claim 31; Fig 4; 108pp; English.
XX XX The present sequence is the human PRO364 protein, encoded by the cDNA
XX XX clone, designated as DNA7365-1206. It is isolated from human small
XX XX intestine tissue cDNA library, identified using probes based on the
XX XX consensus sequence DNA4825, relative to the incyte expressed sequence
XX XX tag (EST) 3003460. This EST has homology to tumour necrosis factor
XX XX receptor (TNFR) family of polypeptides. PRO364 sequence also shows
XX XX homology to members of the TNFR family and mouse G1TR protein. This clone
XX XX is assigned the ATCC deposit No. 209436. PRO364 functions as a neoplastic
XX XX cell growth inhibitor and is used for treating tumours, using an
XX XX effective amount of PRO655, PRO364 and PRO344. This composition is
XX XX especially useful for treatment of human cancers such as breast,
XX XX prostate, colon, lung, renal, ovarian and CNS, leukemia and melanoma
XX XX
XX XX Sequence 241 AA;
XX XX
Query Match 100.0%; Score 1386; DB 3; Length 241;
Best Local Similarity 100.0%; Pred. No. 2.2e-101;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX XX 1 MAQHGWAGAFRALCGLLALCNLSLGRPTGGCGPGRLLLTGTDTARCCRVHTTRCCRD 60
XX XX 1 MAQHGWAGAFRALCGLLALCNLSLGRPTGGCGPGRLLLTGTDTARCCRVHTTRCCRD 60
XX XX 61 YPGEECCSEWDCMCVQPEFHGCGPCCTTCRHHPCPPGQGVQSGKFSFGQICDCASGTF 120
XX XX 61 YPGEECCSEWDCMCVQPEFHGCGPCCTTCRHHPCPPGQGVQSGKFSFGQICDCASGTF 120
XX XX 121 SGHGEHCKPWTCTQFGFLTVPFGNKTNAVCPGSPPAEPGLGWTTVLLVAACVLL 180
XX XX 121 SGHGEHCKPWTCTQFGFLTVPFGNKTNAVCPGSPPAEPGLGWTTVLLVAACVLL 180
XX XX 181 TSAQLGLHIWQLRSQCMWPRETQILLLEVPSTEDARSCQFPEERGERSAEBKGLGLDLW 240

Db 181 TSAQLGLHIWQLRSQCMWPRETQILLLEVPSTEDARSCQFPEERGERSAEBKGLGLDLW 240
QY 241 V 241
Db 241 V 241
RESULT 5
AAB27651
ID AAB27651 standard; protein; 241 AA.
XX XX AAB27651;
XX XX 26-JAN-2001 (first entry)
XX XX Human protein PRO364.
XX XX Cardiovascular; endothelial; angiogenic disorder; PRO179; PRO238; PRO364;
XX XX PRO844; PRO846; PRO1760; PRO205; PRO321; PRO333; PRO840; PRO877; PRO878;
XX XX PRO879; PRO882; PRO885; PRO887; gene therapy.
XX XX Homo sapiens.
XX XX Key Location/Qualifiers
XX XX Peptide 1..25
XX XX FT /label= Signal peptide
XX XX PN WO200053757-A2.
XX XX PD 14-SEP-2000.
XX XX PF 24-FEB-2000; 2000WO-US005004.
XX XX 08-MAR-1999; 99WO-US005028.
XX XX 12-MAR-1999; 99US-0123957P.
XX XX 02-JUN-1999; 99WO-US012252.
XX XX 20-JUL-1999; 99US-0144758P.
XX XX 26-JUL-1999; 99US-0145698P.
XX XX 01-SEP-1999; 99WO-US020111.
XX XX 15-SEP-1999; 99WO-US021090.
XX XX 30-NOV-1999; 99WO-US028313.
XX XX 02-DEC-1999; 99WO-US028409.
XX XX 05-JAN-2000; 2000WO-US000219.
XX XX 18-FEB-2000; 2000WO-US004341.
XX XX 18-FEB-2000; 2000WO-US004342.
XX XX 22-FEB-2000; 2000WO-US004414.
XX XX (GETH) GENENTECH INC.
XX XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Gerritsen ME,
XX XX Goddard A, Gurney AL, Hillan KJ, Marsters SA, Paoni NF, Pitti RM;
XX XX Watanabe CK, Williams PM, Wood WI;
XX XX WPI: 2000-611444/58.
XX XX N-PSDB; AAB99903.
XX XX Novel PRO polypeptides and agonists and antagonists of them, used to
XX XX diagnose and treat cardiovascular, endothelial and angiogenic disorders.
XX XX Claim 71; Fig 6; 181pp; English.
XX XX The present invention relates to methods for stimulating or inhibiting
XX XX angiogenesis and cardiovascularization. The methods involve the use of
XX XX pharmaceutical compositions based on the following proteins, PRO179,
XX XX PRO238, PRO364, PRO844, PRO846, PRO1760, PRO205, PRO321, PRO333, PRO840,
XX XX PRO877, PRO878, PRO879, PRO882, PRO885 or PRO887. These proteins were
XX XX identified by isolating cDNA clones encoding secreted proteins. The
XX XX proteins of the invention may be used to diagnose and treat
XX XX cardiovascular, endothelial or angiogenic disorders. The present sequence
XX XX is one of the proteins of the invention
XX XX Sequence 241 AA;

Query Match 100.0%; Score 1386; DB 3; Length 241;
 Best Local Similarity 100.0%; Pred. No. 2.2e-101;
 Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHGAMGAFRALCGLLALLCALSLGQRTGGCGGPRLLLTGTDAACRCHVHTTRCCRD 60
 DB 1 MAQHGAMGAFRALCGLLALLCALSLGQRTGGCGGPRLLLTGTDAACRCHVHTTRCCRD 60

QY 61 YPGECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSGKFSFGQICDCASGTF 120
 DB 61 YPGECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSGKFSFGQICDCASGTF 120

QY 121 SGHGHGCKPWTDTCTQFGLTVPPGNKTHNAVCPGSPPAEPLGMLTVLLVAACVLLL 180
 DB 121 SGHGHGCKPWTDTCTQFGLTVPPGNKTHNAVCPGSPPAEPLGMLTVLLVAACVLLL 180

QY 181 TSAQLGLHIWQLRSQCMWPRETQLLLEVPSTEDARSCQFPEERGERSAEKGRIGDLW 240
 DB 181 TSAQLGLHIWQLRSQCMWPRETQLLLEVPSTEDARSCQFPEERGERSAEKGRIGDLW 240

QY 241 V 241
 DB 241 V 241

RESULT 6
 AAY95895
 ID AAY95895 standard; protein; 241 AA.
 AC AAY95895;
 XX
 DT 20-NOV-2000 (first entry)
 XX Human tumour necrosis factor receptor-like protein TR11 mutein.
 DE
 XX TR11; human; tumour necrosis factor receptor-like protein;
 KW immunodeficiency; autoimmune disease; rheumatoid arthritis;
 KW immunosuppressive; antirheumatic; antiarthritic; haemostatic;
 KW dermatological; antiinflammatory; therapy; diagnosis; mutein; mutant.
 XX
 OS Homo sapiens.
 XX
 PN WO200050459-A1.
 XX
 PD 31-AUG-2000.
 XX
 PF 23-FEB-2000; 2000WO-US004572.
 XX
 PR 24-FEB-1999; 99US-0121648P.
 PR 13-MAY-1999; 99US-0134172P.
 PR 16-JUL-1999; 99US-0144076P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Ruben SM, Ni J;
 XX
 DR WPI; 2000-572072/53.
 XX
 PT Human tumor necrosis factor receptor-like proteins useful for diagnosis,
 FT prevention and treatment of disease states associated with aberrant cell
 PT survival such as autoimmune disease and rheumatoid arthritis.
 XX
 PS Disclosure; 294-295; 278pp; English.
 XX
 CC The present sequence is that of human tumour necrosis factor receptor-
 CC like protein TR11 (see also AAY95879), a novel protein showing identity
 CC to murine glucocorticoid induced tumour necrosis factor receptor family-
 CC related gene. The invention provides highly conserved TR11, TR11SV1 and
 CC TR11SV2 proteins (see AAY95879-81), as well as vectors, host cells and
 CC recombinant methods for their production. TR11, TR11SV1 and/or TR11SV2
 CC polypeptides are useful for treating, preventing, prognosis and/or
 CC diagnosis of an immunodeficiency, especially common variable

CC immunodeficiency, X-linked agammaglobulinemia, severe combined
 CC immunodeficiency (SCID), Wiskott-Aldrich syndrome or X-linked
 CC immunoglobulin deficiency with hyper IgM. TR11, TR11SV1 and/or TR11SV2
 CC antagonists (e.g. antibodies) are used to treat, prevent, prognosis and/or
 CC diagnosis of an autoimmune disease, especially rheumatoid arthritis, systemic
 CC lupus erythematosus, thrombocytopenia purpura or IGA nephropathy. The
 CC polypeptides, polynucleotides and/or antibodies can be administered to
 CC cells in vitro, ex vivo or in vivo or to a multicellular organism.
 CC Soluble forms of the polypeptides may also be used. Methods for screening
 CC for agonist/antagonist compounds are also provided
 XX
 SQ Sequence 241 AA;
 Query Match 100.0%; Score 1386; DB 3; Length 241;
 Best Local Similarity 100.0%; Pred. No. 2.2e-101;
 Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHGAMGAFRALCGLLALLCALSLGQRTGGCGGPRLLLTGTDAACRCHVHTTRCCRD 60
 DB 1 MAQHGAMGAFRALCGLLALLCALSLGQRTGGCGGPRLLLTGTDAACRCHVHTTRCCRD 60

QY 61 YPGECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSGKFSFGQICDCASGTF 120
 DB 61 YPGECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSGKFSFGQICDCASGTF 120

QY 121 SGHGHGCKPWTDTCTQFGLTVPPGNKTHNAVCPGSPPAEPLGMLTVLLVAACVLLL 180
 DB 121 SGHGHGCKPWTDTCTQFGLTVPPGNKTHNAVCPGSPPAEPLGMLTVLLVAACVLLL 180

QY 181 TSAQLGLHIWQLRSQCMWPRETQLLLEVPSTEDARSCQFPEERGERSAEKGRIGDLW 240
 DB 181 TSAQLGLHIWQLRSQCMWPRETQLLLEVPSTEDARSCQFPEERGERSAEKGRIGDLW 240

QY 241 V 241
 DB 241 V 241

RESULT 7
 AAB24409
 ID AAB24409 standard; protein; 241 AA.
 XX
 AC AAB24409;
 XX
 DT 07-NOV-2000 (first entry)
 XX
 DE Human PRO364 protein sequence SEQ ID NO:117.
 XX
 KW Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;
 KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;
 KW angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic;
 KW cytostatic; gene therapy; vaccine.
 XX
 OS Homo sapiens.
 XX
 PN WO200032221-A2.
 XX
 PD 08-JUN-2000.
 XX
 PF 30-NOV-1999; 99WO-US028313.
 XX
 PR 01-DEC-1998; 98WO-US025108.
 PR 16-DEC-1998; 98US-0112850P.
 PR 12-JAN-1999; 99US-0115554P.
 PR 08-MAR-1999; 99WO-US005028.
 PR 12-MAR-1999; 99US-0123957P.
 PR 28-APR-1999; 99US-0134445P.
 PR 14-MAY-1999; 99US-0134287P.
 PR 02-JUN-1999; 99WO-US012252.
 PR 23-JUN-1999; 99US-0141037P.
 PR 20-JUL-1999; 99US-0144758P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 01-SEP-1999; 99WO-US020111.

```
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-OCT-1999; 99US-0162506P.
XX (GETH ) GENENTECH INC.
PA Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ;
PI Goddard A, Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF;
PI Smith V, Watanabe CK, Williams PM, Wood WI;
XX
XX WPI; 2000-412154/35.
XX N-PSDB; AAA77604.
XX
XX Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing
XX and treating diagnosing a cardiovascular, endothelial or angiogenic
XX disorders in mammals.
XX
XX Claim 72; Fig 44; 315pp; English.
XX
XX The present invention describes nucleic acids encoding PRO polypeptides
XX useful for preventing, diagnosing and treating diagnosing a
XX cardiovascular, endothelial or angiogenic disorder in mammals by
XX modulating cell proliferation, angiogenesis and cardiovascularisation,
XX and for identifying agonists and antagonists of these processes. The
XX nucleic acids and the proteins they encode may be used in the prevention,
XX treatment and diagnosis of diseases associated with inappropriate PRO
XX expression such as cardiovascular, endothelial or angiogenic disorders in
XX mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For
XX example, the nucleic acids (NCs) and vectors containing them and the PRO
XX polypeptide may be used to treat disorders associated with decreased PRO
XX expression. AAA77510 to AAA77721 and AAB24388 to AAB24435 represent
XX nucleotide and protein sequences used in the exemplification of the
XX present invention
XX
XX Sequence 241 AA;
XX
XX Query Match 100.0%; Score 1386; DB 3; Length 241;
XX Best Local Similarity 100.0%; Pred. No. 2.2e-101;
XX Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAQHGGAMGAFRALCGIALICALSLGQRTGGPGCGPGRLLLTGTGDARCCRVHTTRCCRD 60
DB 1 MAQHGGAMGAFRALCGIALICALSLGQRTGGPGCGPGRLLLTGTGDARCCRVHTTRCCRD 60
QY 61 YPGECCSEBDCMCVQPEFHCGDPCCCTCRHHPCPGQVQSGKFSFGQICDASGTF 120
DB 61 YPGECCSEBDCMCVQPEFHCGDPCCCTCRHHPCPGQVQSGKFSFGQICDASGTF 120
QY 121 SGHGEHCKPWTDTCTQGFLLTVPGNKTHNAVCPGSPPAEPGLGMLTVLLAAACVLL 180
DB 121 SGHGEHCKPWTDTCTQGFLLTVPGNKTHNAVCPGSPPAEPGLGMLTVLLAAACVLL 180
QY 181 TSAQLGLHIWQLRSQCMWRETQLLEVPSTEDARSCQFPPEERGERSAEBKRGRLDLW 240
DB 181 TSAQLGLHIWQLRSQCMWRETQLLEVPSTEDARSCQFPPEERGERSAEBKRGRLDLW 240
QY 241 V 241
DB 241 V 241
XX
XX RESULT 8
XX ID AAB47054 standard; protein; 241 AA.
XX AC AAB47054;
XX DT 08-MAY-2001 (first entry)
XX DE Human PRO364.
```

```
XX KW PRO364; human; glucocorticoid-induced tumor necrosis factor; receptor;
XX HGTR; ligand; hGTR; PRO175; tumour necrosis factor receptor; TNFR;
XX human umbilical vein endothelial cell; HUVEC; cardiac hypertrophy;
XX myocardial infarction; PGF 2alpha; trauma; cancer; angiogenesis;
XX age-related macular degeneration; antibody; periodontal disease;
XX vascular-related drug targeting; atherosclerosis; hypertension;
XX inflammatory vasculitides; Reynaud's disease; aneurysm;
XX arterial restenosis; thrombophlebitis; tumor angiogenesis; lung; liver;
XX fibrosis; neuropathy; rheumatoid arthritis.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..26
XX /note= "Potential signal peptide"
XX
XX Modified-site 146
XX /note= "N-glycosylated"
XX
XX Domain 162..180
XX /note= "Potential transmembrane domain"
XX
XX WO200103720-A2.
XX
XX 18-JAN-2001.
XX
XX 11-JUL-2000; 2000WO-US018867.
XX
XX 12-JUL-1999; 99US-0143304P.
XX (GETH ) GENENTECH INC.
XX
XX Williams PM, Gerritsen ME;
XX
XX WPI; 2001-138257/14.
XX N-PSDB; AAC85433.
XX
XX Composition for diagnosing and treating cardiovascular, endothelial and
XX angiogenic disorders, comprises a PRO364 or PRO175 polypeptide.
XX
XX Claim 1; Fig 1; 76pp; English.
XX
XX This sequence represents PRO364 polypeptide, which is a human gluco-
XX corticoid-induced tumor necrosis factor receptor (hGTR). The
XX corresponding ligand (hGTR), PRO175, is given in AAB47056. PRO364 and
XX PRO175 may be used in a mixture with a cardiovascular, endothelial,
XX angiogenic or angiostatic agent for the treatment of a cardiovascular,
XX endothelial, angiostatic or angiostatic disorder. The PRO364 cDNA sequence
XX was isolated from an expressed sequence tag (EST) database as having
XX homology to members of the tumour necrosis factor receptor (TNFR) family
XX of polypeptides. The PRO175 cDNA sequence was isolated from a library of
XX cDNA fragments derived from human umbilical vein endothelial cells
XX (HUVEC). Administering an effective amount of PRO364 or PRO175 or their
XX antagonists is useful for treating cardiac hypertrophy (which is
XX initiated by myocardial infarction and characterized by the presence of
XX an elevated level of PGF 2alpha), trauma, a cancer, or age-related
XX macular degeneration in a human. Administering a therapeutically
XX effective amount of an antibody that binds PRO364 or PRO175 is useful for
XX inhibiting angiogenesis induced by PRO364 or PRO175 in a human suffering
XX from a tumor or a retinal disorder. PRO364 or PRO175, or their
XX antagonists, are useful for vascular-related drug targeting or as
XX therapeutic targets for the treatment or prevention of atherosclerosis,
XX hypertension, inflammatory vasculitides, Reynaud's disease, aneurysms,
XX arterial restenosis, thrombophlebitis, tumor angiogenesis, gut protection
XX or regeneration and treatment of lung or liver fibrosis, periodontal
XX diseases, attraction of bone-forming cells, central and peripheral
XX nervous system disease and neuropathies and rheumatoid arthritis
XX
XX Sequence 241 AA;
XX
XX Query Match 100.0%; Score 1386; DB 4; Length 241;
XX Best Local Similarity 100.0%; Pred. No. 2.2e-101;
XX Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 MAQHGWGAFRALCGLALLCALSLGQRTGPGCGCPGRLLLGTGTDARCCRVHTTRCCRD 60
Db 1 MAQHGWGAFRALCGLALLCALSLGQRTGPGCGCPGRLLLGTGTDARCCRVHTTRCCRD 60
QY 61 YPGECCSEWDCMCVQPEPHCGDPCCCTCRHHPCPPGQVQSGKPSFGFCIDCASGTF 120
Db 61 YPGECCSEWDCMCVQPEPHCGDPCCCTCRHHPCPPGQVQSGKPSFGFCIDCASGTF 120
QY 121 SGGHEGCHKPWTCTQFGFLTVPFGNKNHNAVCPGSPPAEPLGMLTVVLLAAACVLL 180
Db 121 SGGHEGCHKPWTCTQFGFLTVPFGNKNHNAVCPGSPPAEPLGMLTVVLLAAACVLL 180
QY 181 TSAQLGLHQLWLSQCMWPRETQLLEVPSTEDARSCQFPPEERGERSAEKRGIDLW 240
Db 181 TSAQLGLHQLWLSQCMWPRETQLLEVPSTEDARSCQFPPEERGERSAEKRGIDLW 240
QY 241 V 241
Db 241 V 241

RESULT 9
AAB20115
ID AAB20115 standard; protein; 241 AA.
AC AAB20115;
XX
XX 30-APR-2001 (first entry)
XX Human immunostimulant PRO364.
XX
XX PRO364; UNQ319; human; immune disease; autoimmune disease; antirheumatic;
KW antiarthritic; antiinflammatory; antianaemic; immunosuppressive;
KW antithyroid; antidiabetic; neuroprotective; hepatotropic; virucide;
KW dermatological; antipsoriatic; antiasthmatic; antiallergic;
KW immunostimulant.
XX
XX Homo sapiens.
XX
XX Key
XX Peptide 1. .25 Location/Qualifiers
XX /label= Signal_peptide
XX Modified-site 5. .11
XX /note= "N-myristoylation site"
XX Modified-site 8. .14
XX /note= "N-myristoylation site"
XX Modified-site 25. .31
XX /note= "N-myristoylation site"
XX Protein 26. .241
XX /label= Mature_protein
XX Modified-site 30. .36
XX /note= "N-myristoylation site"
XX Modified-site 33. .39
XX /note= "N-myristoylation site"
XX Modified-site 118. .124
XX /note= "N-myristoylation site"
XX Modified-site 122. .128
XX /note= "N-myristoylation site"
XX Modified-site 146. .150
XX /note= "Asn is N-glycosylated"
XX Modified-site 156. .162
XX /note= "N-myristoylation site"
XX Domain 163. .183
XX /note= "transmembrane domain"
XX Peptide 166. .177
XX /note= "prokaryotic membrane lipoprotein lipid attachment site"
XX Peptide 171. .193
XX /note= "leucine zipper pattern"
XX
XX WO200105972-A1.
XX
XX 25-JAN-2001.
```

```
XX 15-MAR-2000; 2000WO-US006884.
XX 20-JUL-1999; 99US-0144758P.
XX (GETH ) GENENTECH INC.
XX Ashkenazi AJ, Baker KP, Pong S, Goddard A, Godowski PJ, Tumas D;
PI Gurney AL, Hillan KJ, Mark MR, Marsters SA, Pitti RM, Watanabe CK, Wood WT;
PI Watanabe CK, Wood WT;
XX WPI; 2001-103149/11.
DR N-PSDB; AAF30057.
XX
XX New PRO polypeptides, nucleic acids and (ant)agonists, useful for
PT diagnosing and treating immune-related disorders, such as multiple
PT sclerosis, rheumatoid arthritis and diabetes.
XX
XX Claim 20; Fig 16; 127pp; English.
XX
XX The present sequence is that of novel human immunomodulator PRO364
XX (UNQ319), as deduced from cDNA (see AAF30057) isolated from a small
XX intestine library. PRO364 (26 kDa, pI 6.34) shows sequence homology to
XX mouse G1TR protein and may be its human counterpart. The invention
XX provides polynucleotides (see AAF30050-62) encoding novel human PRO
XX proteins (see AAB20108-20) including PRO364. Claimed compositions
XX comprising these proteins or their agonists are useful for increasing
XX infiltration of inflammatory cells into a tissue of a mammal, stimulating
XX or enhancing an immune response, or increasing the proliferation of T-
XX lymphocytes in a mammal in response to an antigen. Claimed compositions
XX comprising a PRO polypeptide or its antagonist have the opposite effect.
XX A claimed method for treating an immune related disorder, such as a T
XX cell disorder, involves administering a PRO polypeptide, an agonist
XX antibody or an antagonist antibody. The disorder is selected from
XX systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
XX juvenile chronic arthritis, spondyloarthritis, systemic sclerosis,
XX idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
XX vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
XX thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal
XX disease, demyelinated diseases (such as multiple sclerosis), autoimmune
XX chronic active hepatitis, primary biliary cirrhosis, granulomatous
XX hepatitis, sclerosing cholangitis, inflammatory bowel disease (ulcerative
XX colitis and Crohn's disease), gluten-sensitive enteropathy, Whipple's
XX disease, (auto)immune-mediated skin diseases (such as bullous skin
XX disease, erythema multiforme and psoriasis), allergic diseases (such as
XX asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity and
XX urticaria), immunologic diseases of the lung and transplantation
XX associated diseases (such as graft rejection and graft-versus-host
XX disease) (all claimed). Claimed methods of diagnosing these disorders
XX comprise detecting the level of expression of the PRO gene. Also claimed
XX are a method of identifying a compound capable of inhibiting the
XX expression or activity of the PRO polypeptide, vectors, host cells,
XX antibodies, and a method of stimulating the proliferation of T
XX lymphocytes using PRO364
XX
XX Sequence 241 AA;
XX
XX Query Match 100.0%; Score 1386; DB 4; Length 241;
XX Best Local Similarity 100.0%; Pred. No. 2.2e-101;
XX Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAQHGWGAFRALCGLALLCALSLGQRTGPGCGCPGRLLLGTGTDARCCRVHTTRCCRD 60
Db 1 MAQHGWGAFRALCGLALLCALSLGQRTGPGCGCPGRLLLGTGTDARCCRVHTTRCCRD 60
QY 61 YPGECCSEWDCMCVQPEPHCGDPCCCTCRHHPCPPGQVQSGKPSFGFCIDCASGTF 120
Db 61 YPGECCSEWDCMCVQPEPHCGDPCCCTCRHHPCPPGQVQSGKPSFGFCIDCASGTF 120
QY 121 SGGHEGCHKPWTCTQFGFLTVPFGNKNHNAVCPGSPPAEPLGMLTVVLLAAACVLL 180
Db 121 SGGHEGCHKPWTCTQFGFLTVPFGNKNHNAVCPGSPPAEPLGMLTVVLLAAACVLL 180
```

QY 181 TSAQLGLHIWQLRSQCMWPRETQLLEVPSTEDARSCQFPEERGERSAEKGRLGDLW 240
 DB 181 TSAQLGLHIWQLRSQCMWPRETQLLEVPSTEDARSCQFPEERGERSAEKGRLGDLW 240
 QY 241 V 241
 DB 241 V 241

RESULT 10
 AAB53090
 ID AAB53090 standard; protein; 241 AA.
 AC AAB53090;
 XX
 XX 28-FEB-2001 (first entry)
 XX Human angiogenesis-associated protein PRO364, SEQ ID NO:142.
 XX Human; angiogenesis-associated protein; PRO; endothelial cell growth;
 KW cardiac hypertrophy; cardiovascular disorder; endothelial disorder;
 KW angiogenic disorder; atherosclerosis; osteoporosis; hypertension;
 KW myocardial infarction; diabetic retinopathy; rheumatoid arthritis;
 KW Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;
 KW Alzheimer's disease; Huntington's disease; stroke; drug screening;
 KW Gene therapy; transgenic animal.
 XX
 OS Homo sapiens.
 XX
 XX WO200053753-A2.
 XX
 XX 14-SEP-2000.
 XX
 XX 05-JAN-2000; 2000WO-US000219.
 XX
 XX 08-MAR-1999; 99WO-US005028.
 XX 12-MAR-1999; 99US-0123957P.
 XX 14-MAY-1999; 99US-0134287P.
 XX 02-JUN-1999; 99WO-US012252.
 XX 23-JUN-1999; 99US-0141037P.
 XX 20-JUL-1999; 99US-0144758P.
 XX 26-JUL-1999; 99US-0145698P.
 XX 01-SEP-1999; 99WO-US020111.
 XX 08-SEP-1999; 99WO-US020594.
 XX 15-SEP-1999; 99WO-US021090.
 XX 15-SEP-1999; 99WO-US021547.
 XX 05-OCT-1999; 99WO-US023089.
 XX 30-NOV-1999; 99WO-US028313.
 XX 30-NOV-1999; 99WO-US028409.
 XX 02-DEC-1999; 99WO-US028564.
 XX 02-DEC-1999; 99WO-US028565.
 XX
 XX (GETH) GENENTECH INC.
 XX
 XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;
 PI Godowski PJ, Gurney AL, Hillan KO, Kuo SS, Mark MR, Marsters SA;
 PI Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;
 XX
 XX WPI: 2001-090793/10.
 XX N-PSDB; AAC97479.
 XX
 XX New isolated nucleic acid for producing a PRO polypeptide, analyzing
 PT genetic disorders and treating cardiovascular, endothelial or angiogenic
 PT disorders, such as atherosclerosis, wounds or cancer.
 XX
 XX Claim 69; Fig 54; 293pp; English.
 XX
 XX The invention relates to novel human angiogenesis-associated proteins
 CC designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding
 CC PRO proteins. The invention also relates to vectors and host cells
 CC comprising a PRO nucleic acid, the recombinant production of a PRO
 CC protein, PRO antibodies specific for a PRO protein, fusion proteins
 CC comprising a PRO protein, agonists or antagonists of a PRO protein, and

CC compounds which inhibit the expression of a PRO gene. The invention
 CC additionally encompasses methods of identifying modulators of PRO
 CC expression or activity; diagnosing a cardiovascular, endothelial or
 CC angiogenic disorder, or a susceptibility to such a disorder by detecting
 CC mutations in a PRO gene, or the expression level of a PRO gene within a
 CC particular tissue; treating a cardiovascular, endothelial or angiogenic
 CC disorder via the administration of a PRO protein, PRO nucleic acid, or
 CC PRO agonist or antagonist; a retroviral gene therapy vector comprising a
 CC PRO nucleic acid; and methods of inhibiting or stimulating endothelial
 CC cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the
 CC administration of a PRO protein, or an agonist or antagonist thereof. PRO
 CC nucleic acids, PRO proteins, antibodies against PRO proteins, PRO
 CC agonists and PRO antagonists may be used as therapeutic agents to treat
 CC cardiovascular, endothelial or angiogenic disorders, such as
 CC atherosclerosis, osteoporosis, myocardial infarction, hypertension,
 CC diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,
 CC endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's
 CC disease, or stroke. PRO nucleic acids are additionally useful in the
 CC recombinant production of PRO proteins, as hybridisation probes to screen
 CC libraries to isolate cDNAs with sequence identity to PRO proteins, to map
 CC genes encoding PRO proteins, to analyse genetic disorders, and in gene
 CC therapy. PRO nucleic acids can also be used to produce transgenic animals
 CC useful for the development and screening of potential therapeutic agents.
 CC The present sequence represents a PRO protein of the invention
 XX
 XX Sequence 241 AA;
 SQ

Query Match 100.0%; Score 1386; DB 4; Length 241;
 Best Local Similarity 100.0%; Pred. No. 2.2e-101;
 Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHGAMGAFRALCGLALLCALSLGQRTGPGCGPGRLLLTGTGDARCCRVHTTCCRD 60
 DB 1 MAQHGAMGAFRALCGLALLCALSLGQRTGPGCGPGRLLLTGTGDARCCRVHTTCCRD 60
 QY 61 YPGECCSEWDCMCVQPEFHGCDPCTTCRHHPCPPGQVQSQGKFSFGFCQIDCASGTF 120
 DB 61 YPGECCSEWDCMCVQPEFHGCDPCTTCRHHPCPPGQVQSQGKFSFGFCQIDCASGTF 120
 QY 121 SGGHEGHCKPMTDCTQFGFLTVPFGKNTNNAVCVPGSPAPPLGWLTVVLLAAACVLL 180
 DB 121 SGGHEGHCKPMTDCTQFGFLTVPFGKNTNNAVCVPGSPAPPLGWLTVVLLAAACVLL 180
 QY 181 TSAQLGLHIWQLRSQCMWPRETQLLEVPSTEDARSCQFPEERGERSAEKGRLGDLW 240
 DB 181 TSAQLGLHIWQLRSQCMWPRETQLLEVPSTEDARSCQFPEERGERSAEKGRLGDLW 240
 QY 241 V 241
 DB 241 V 241

RESULT 11
 AAB47289
 ID AAB47289 standard; protein; 241 AA.
 XX
 XX AAB47289;
 XX
 XX 22-AUG-2001 (first entry)
 XX
 XX PRO364 polypeptide.
 XX
 XX PRO; type II transmembrane protein; tumour necrosis factor; stroke;
 KW heart hypertrophy; cardiovascular; endothelial; angiogenic; disorder;
 KW myocardial infarction; cardiac hypertrophy; PGF 2alpha; trauma; bone;
 KW cancer; age-related macular degeneration; wound; burn; hypertension;
 KW diabetes mellitus; osteoporosis; ischaemia; atherosclerosis; psoriasis;
 KW rheumatoid arthritis; Crohn's disease; amyotrophic lateral sclerosis;
 KW endometriosis; angina; neoplasms; periodontal disease; cartilage; TNF;
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease.
 XX
 OS Homo sapiens.
 XX

Key Location/Qualifiers
Peptide 1..25 /label= Signal peptide
Modified-site 5..11 /label= N-myristoylation site
Modified-site 8..14 /label= N-myristoylation site
Modified-site 25..31 /label= N-myristoylation site
Protein 26..241 /label= N-myristoylation site
Modified-site 30..36 /label= Mature PRO364
Modified-site 33..39 /label= N-myristoylation site
Modified-site 118..124 /label= N-myristoylation site
Modified-site 122..128 /label= N-myristoylation site
Modified-site 146..150 /label= N-linked glycosylation site
Modified-site 156..162 /label= N-myristoylation site
Domain 162..180 /label= Potential transmembrane domain
Binding-site 166..177 /label= Prokaryotic membrane lipoprotein attachment site
Domain 171..193 /label= Leucine zipper
WO20010464-A1.
07-JUN-2001.
11-AUG-2000; 2000WO-US022031.
30-NOV-1999; 99WO-US028313.
30-NOV-1999; 99WO-US028409.
05-JAN-2000; 2000WO-US000219.
24-FEB-2000; 2000WO-US005004.
15-MAR-2000; 2000WO-US006884.
30-MAR-2000; 2000WO-US008439.
17-MAY-2000; 2000WO-US013705.
30-MAY-2000; 2000WO-US014941.
28-JUL-2000; 2000WO-US020710.
(GETH) GENENTECH INC.
Ashkenazi AJ, Baker KP, Ferrara N, Godowski PJ, Gurney AL;
Hillan KJ, Mark MR, Marsters SA, Paoni NF, Pitti RM, Wood WI;
WPI; 2001-381383/40.
N-PSDB; AAC85947.
Isolated PRO polypeptide useful in treating and diagnosing a
cardiovascular, endothelial or angiogenic disorder e.g. cancer, diabetes
mellitus, myocardial infarction, arthritis.
Claim 56; Fig 6; 144pp; English.
The sequences given in ABA47287-90 show PRO polypeptides, PRO175 shows
type II transmembrane protein typology, and portions of PRO364 show
homology to members of the tumour necrosis factor (TNF) family, thereby
indicating that it may be a novel member of the TNF family. PRO175 and
PRO185 stimulated heart hypertrophy. PRO cDNA's may be used to identify a
compound that inhibits PRO, diagnosing a cardio-vascular, endothelial or
angiogenic disorder in a mammal by detecting PRO cDNA, treating
cardiovascular, endothelial or angiogenic disorder in a mammal, and
inducing cardiac hypertrophy or inhibiting endothelial cell growth or
angiogenesis in a mammal. The mammal is a human which has suffered
myocardial infarction, cardiac hypertrophy characterized by the presence
of elevated PGP 2alpha, trauma, cancer or age-related macular
degeneration. Trauma includes wounds or burns. Other treatable diseases

CC include diabetes mellitus, osteoporosis, ischaemia, hypertension,
CC rheumatoid arthritis, Crohn's disease, atherosclerosis, psoriasis,
CC endometriosis, angina, neoplasms, periodontal disease, bone and cartilage
CC repair, Alzheimer's disease, Parkinson's disease, Huntington's disease,
CC amyotrophic lateral sclerosis, and stroke
XX
SQ Sequence 241 AA;
Query Match 100.0%; Score 1386; DB 4; Length 241;
Best Local Similarity 100.0%; Pred. No. 2.2e-101;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAQHGAMGAFRALCGALLCALSLGQRTGPGCGPGRLLLTGTDDARCCRVHTRCCRD 60
DB 1 MAQHGAMGAFRALCGALLCALSLGQRTGPGCGPGRLLLTGTDDARCCRVHTRCCRD 60
QY 61 YPGECCSEWDCMCVQPEFHCGDPCTTCRHHPCPPGQGVQSGKFSFGQCIDCASGTF 120
DB 61 YPGECCSEWDCMCVQPEFHCGDPCTTCRHHPCPPGQGVQSGKFSFGQCIDCASGTF 120
QY 121 SGHGHGCHKPMTDCTQFGFLTVPFGNKTNAVCVPGSPPAEPLGMLTVVLLAAVACVLL 180
DB 121 SGHGHGCHKPMTDCTQFGFLTVPFGNKTNAVCVPGSPPAEPLGMLTVVLLAAVACVLL 180
QY 181 TSAQLGLHIWQLRSQCMMPRETQLLEVPSTEDARSCQFPPEERGERSAEKGRLGLDW 240
DB 181 TSAQLGLHIWQLRSQCMMPRETQLLEVPSTEDARSCQFPPEERGERSAEKGRLGLDW 240
QY 241 V 241
DB 241 V 241
RESULT 12
AAB50982
ID AAB50982 standard; protein; 241 AA.
XX
AC AAB50982;
XX
DT 21-MAR-2001 (first entry)
XX
DE Human PRO364 protein.
XX
KW Human; PRO; cardiac; antiangiogenic; antiarteriosclerotic; hypotensive;
KW vasotropic; antiarthritis; antiarthritic; antiinflammatory; cytostatic;
KW vulnary; antianginal; gene therapy; cardiovascular disease;
KW endothelial disorder; angiogenic disorder; cancer; periodontal disease;
KW wound healing.
XX
OS Homo sapiens.
XX
PN WO200073445-A2.
XX
PD 07-DEC-2000.
XX
PF 17-MAY-2000; 2000WO-US013705.
XX
PR 02-JUN-1999; 99WO-US012252.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 01-SEP-1999; 99WO-US020111.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US000365.
PR 18-FEB-2000; 2000WO-US000431.
PR 18-FEB-2000; 2000WO-US000432.
PR 24-FEB-2000; 2000WO-US000504.

PR 02-MAR-2000; 2000WO-US005841.
 PR 10-MAR-2000; 2000WO-US006319.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 21-MAR-2000; 2000WO-US007532.
 PR 30-MAR-2000; 2000WO-US008439.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Gershtsen ME;
 PI Goddard A, Godowski PJ, Gurney AL, Kuo SS, Mark MR, Marsters SA;
 PI Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;
 XX
 DR WPI; 2001-025251/03.
 DR N-PSDB; AAC90566.
 XX
 PT Seventeen nucleic acids encoding PRO polypeptides which are useful in
 PT diagnosis and treatment of cardiovascular, endothelial or angiogenic
 PT disorders in a mammal.
 XX
 XX Claim 71; Fig 8; 182pp; English.
 XX
 CC The present sequence is one of seventeen novel PRO polypeptides. The PRO
 CC nucleic acids, polypeptides, agonists and antagonists are useful for
 CC treating cardiovascular, endothelial or angiogenic disorders in a mammal.
 CC Examples of these disorders include cardiac hypertrophy, trauma, cancer,
 CC age-related macular degeneration, atherosclerosis, hypertension, arterial
 CC infarctions, Reynaud's disease, rheumatoid arthritis, angina, myocardial
 CC stenosis, thrombophlebitis and lymphangitis. The PRO polypeptides and
 CC antagonists are also used to prevent tumour angiogenesis and for treating
 CC periodontal diseases. They are also used to stimulate wound healing and
 CC tissue regeneration. The PRO nucleic acids, polypeptides and anti-PRO
 CC antibodies are useful for diagnosing a cardiovascular, endothelial or
 CC angiogenic disorder
 XX
 SQ Sequence 241 AA;
 Query Match 100.0%; Score 1386; DB 4; Length 241;
 Best Local Similarity 100.0%; Pred. No. 2.2e-101;
 Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAQHGAWGAFRALCGLALLCALSLGORTGPGCGPGRLLLTGTDAACRCRVHTRCCRD 60
 DB 1 MAQHGAWGAFRALCGLALLCALSLGORTGPGCGPGRLLLTGTDAACRCRVHTRCCRD 60
 QY 61 YPGEECCSEWDCMCVQPEFHGCDPCCTTCRHHPCPGQVQSGKFSFGFCIDCASGTF 120
 DB 61 YPGEECCSEWDCMCVQPEFHGCDPCCTTCRHHPCPGQVQSGKFSFGFCIDCASGTF 120
 QY 121 SGHGHGCHKPWTDTQFGFLTVPFGNKTNAVCPGSPPAEPLGWLTVVLLVAACVLLL 180
 DB 121 SGHGHGCHKPWTDTQFGFLTVPFGNKTNAVCPGSPPAEPLGWLTVVLLVAACVLLL 180
 QY 181 TSAQLGLHIWQLRSQCMWPRETOLLLEVPSTEDARSCFPPEERGERSAEKGRGLDW 240
 DB 181 TSAQLGLHIWQLRSQCMWPRETOLLLEVPSTEDARSCFPPEERGERSAEKGRGLDW 240
 QY 241 V 241
 DB 241 V 241
 RESULT 13
 AAB50910
 ID AAB50910 standard; protein; 241 AA.
 XX
 AC AAB50910;
 XX
 DT 21-MAR-2001 (first entry)
 DE Human PRO364 protein.
 XX
 XX Human; PRO; antiinflammatory; dermatological; antiarthritic;
 XX antirheumatic; cardiant; antianaemic; immunosuppressive; antithyroid;

KW antidiabetic; nootropic; neuroprotective; hepatotropic; virucide;
 KW analleergic; antiasthmatic; immune related disorder;
 KW hepatobiliary disease; autoimmune disease; allergy.
 XX
 OS Homo sapiens.
 XX
 FN WO200073452-A2.
 XX
 PD 07-DEC-2000.
 XX
 PF 02-JUN-2000; 2000WO-US015264.
 XX
 PR 02-JUN-1999; 99WO-US012252.
 PR 20-JUL-1999; 99US-0144732P.
 PR 28-JUL-1999; 99US-0144758P.
 PR 01-SEP-1999; 99WO-US020111.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 29-OCT-1999; 99US-0162506P.
 PR 30-NOV-1999; 99WO-US028313.
 PR 01-DEC-1999; 99WO-US028634.
 PR 02-DEC-1999; 99WO-US028551.
 PR 02-DEC-1999; 99WO-US028565.
 PR 20-DEC-1999; 99US-0170262P.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US004914.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 03-MAR-2000; 2000US-0187202P.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 21-MAR-2000; 2000WO-US007532.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Chan B, Goddard A, Godowski PJ;
 PI Gurney AL, Hebert C, Henzel W, Kabakoff RC, Shelton DL, Tumas D;
 PI Watanabe CK, Wood WI;
 XX
 DR WPI; 2001-025253/03.
 DR N-PSDB; AAC91469.
 XX
 PT Thirty three nucleic acids encoding PRO polypeptides which are useful in
 PT the diagnosis and treatment of immune related disorders, e.g. systemic
 PT lupus erythematosus, rheumatoid arthritis, osteoarthritis, thyroiditis
 PT and diabetes mellitus.
 XX
 XX Claim 58; Fig 18; 218pp; English.
 XX
 CC The present sequence is one of thirty three novel PRO polypeptides. The
 CC PRO polypeptides, anti-PRO antibodies, agonists and antagonists are
 CC useful for treating and diagnosing immune related disorders such as
 CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
 CC juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis,
 CC idiopathic inflammatory myopathies, Sjogren's syndrome, systemic
 CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
 CC thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal
 CC disease, demyelinating diseases of the central and peripheral nervous
 CC systems (such as multiple sclerosis, idiopathic demyelinating
 CC polyneuropathy or Guillain-Barre syndrome, and chronic inflammatory
 CC demyelinating polyneuropathy), hepatobiliary diseases (such as
 CC infectious, autoimmune chronic active hepatitis, primary biliary

CC cirrhosis, granulomatous hepatitis and sclerosing cholangitis),
CC inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's
CC disease, autoimmune or immune-mediated skin diseases (such as bullous
CC skin diseases, erythema multiforme, contact dermatitis, psoriasis),
CC allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,
CC food hypersensitivity and urticaria), immunological diseases of the lung
CC (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis and
CC hypersensitivity pneumonitis), transplantation associated diseases
CC including graft rejection and graft-versus-host diseases
XX
SQ Sequence 241 AA;
Query Match 100.0%; Score 1386; DB 4; Length 241;
Best Local Similarity 100.0%; Pred. No. 2.2e-101;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAQHGMGAFRALCGLALCALSLGQRTGGPGCGPRLLLGTGTDAACRVRHTRCCRD 60
Db 1 MAQHGMGAFRALCGLALCALSLGQRTGGPGCGPRLLLGTGTDAACRVRHTRCCRD 60
QY 61 YPGECCSEWDCMCVQPEPHCGDPCCCTCRHHPCPPGQVQSGKFSFGQCIDCASGTF 120
Db 61 YPGECCSEWDCMCVQPEPHCGDPCCCTCRHHPCPPGQVQSGKFSFGQCIDCASGTF 120
QY 121 SGHEGHCKPWTDTCTQFGLTVFPGKNTNANVCVPGSPPAEPGLGWLTVLLVAACVLL 180
Db 121 SGHEGHCKPWTDTCTQFGLTVFPGKNTNANVCVPGSPPAEPGLGWLTVLLVAACVLL 180
QY 181 TSAQLGLHIWQLRSQCMWPRETQLLEVPSTEDARSCQPFPEERGERSAEKGRLGLDW 240
Db 181 TSAQLGLHIWQLRSQCMWPRETQLLEVPSTEDARSCQPFPEERGERSAEKGRLGLDW 240
QY 241 V 241
Db 241 V 241
RESULT 14
AAE28161
ID AAE28161 standard; protein; 241 AA.
AC AAE28161;
XX
DT 27-DEC-2002 (first entry)
DE Human TR11 receptor protein #2.
XX
KW Human; tumour necrosis factor receptor; TNF; allergic encephalomyelitis;
KW autoimmune disease; autoimmune haemolytic anaemia; multiple sclerosis;
KW systemic lupus erythematosus; Goodpasture's syndrome; diabetes mellitus;
KW rheumatoid arthritis; Sjogren's syndrome; scleroderma; immunodeficiency;
KW urticaria; DiGeorge anomaly; natural killer deficiency; asthma; allergy;
KW inflammatory condition; respiratory disorder; graft-versus-host disease;
KW transplantation rejection; type II collagen-induced arthritis; cancer;
KW cardiovascular disorder; atherosclerosis; gastrointestinal disorder;
KW myocarditis; inflammatory bowel disease; traumatic brain injury; stroke;
KW Alzheimer's disease; inflammation; trauma; septic shock; thrombolytic;
KW gout; haemostatic; blood coagulation disorder; blood platelet disorder;
KW thrombocytopaenia; wound; trauma; surgery; gene therapy; immuno therapy;
KW TR11 receptor.
XX
OS Homo sapiens.
XX
PN US2002098525-A1.
XX
PD 25-JUL-2002.
XX
PF 27-JUL-2001; 2001US-00915593.
XX
PR 21-OCT-1997; 97US-0063212P.
PR 21-OCT-1998; 98US-00176200.
PR 24-FEB-1999; 99US-0121648P.
PR 13-MAY-1999; 99US-0134172P.
PR

PR 16-JUL-1999; 99US-0144076P.
PR 23-FEB-2000; 2000US-00512363.
PR 28-JUL-2000; 2000US-0221577P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Ni J, Ruben SM;
XX PI
XX WPI; 2002-673824/72.
XX
DR Novel antibody or its portion which specifically binds to two tumor
PT necrosis factor receptor-related protein splice variants, TR11SV1 and
PT TR11SV2, useful for treating autoimmune hemolytic anemia, and
PT Goodpasture's syndrome.
XX
PS Disclosure; Page 122; 135pp; English.
XX
CC The present invention relates to novel antibodies or their portion which
CC specifically bind tumour necrosis factor (TNF) receptor-related protein
CC splice variants, TR11SV1 or TR11SV2. Sequences of the invention are
CC useful for treating, detecting and/or preventing diseases, disorders or
CC conditions associated with aberrant expression and/or activity of TR11,
CC TR11SV1 and TR11SV2 polypeptides, e.g., autoimmune diseases such as
CC auto-immune haemolytic anaemia, allergic encephalomyelitis, multiple
CC sclerosis, systemic lupus erythematosus, Goodpasture's syndrome, diabetes
CC mellitus, rheumatoid arthritis, Sjogren's syndrome, scleroderma with anti-
CC collagen antibodies, urticaria, conditions associated with immuno-
CC deficiency e.g. T-cell related deficiencies such as DiGeorge anomaly,
CC natural killer deficiency, inflammatory conditions such as respiratory
CC disorders (e.g. asthma, allergy), allergic reactions such as asthma,
CC graft-versus-host-disease, transplantation rejections, type II collagen-
CC induced arthritis, cancers (ovarian lung, bladder or liver cancer),
CC cardiovascular disorders (atherosclerosis, myocarditis), gastrointestinal
CC disorders (inflammatory bowel disease), central nervous system disorders
CC (e.g. traumatic brain injury, Alzheimer's disease, stroke) and disorders
CC characterised by inflammation (e.g. gout, trauma, septic shock). They are
CC used for modulating haemostatic or thrombolytic activity and thus is used
CC for treating blood coagulation disorders, the blood platelet disorders
CC (e.g. thrombocytopaenia) or wounds resulting from trauma, surgery or
CC other causes. Polynucleotides of the invention are useful in gene therapy
CC and immuno therapy. The present sequence is human TR11 receptor protein
XX
SQ Sequence 241 AA;
Query Match 100.0%; Score 1386; DB 5; Length 241;
Best Local Similarity 100.0%; Pred. No. 2.2e-101;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAQHGMGAFRALCGLALCALSLGQRTGGPGCGPRLLLGTGTDAACRVRHTRCCRD 60
Db 1 MAQHGMGAFRALCGLALCALSLGQRTGGPGCGPRLLLGTGTDAACRVRHTRCCRD 60
QY 61 YPGECCSEWDCMCVQPEPHCGDPCCCTCRHHPCPPGQVQSGKFSFGQCIDCASGTF 120
Db 61 YPGECCSEWDCMCVQPEPHCGDPCCCTCRHHPCPPGQVQSGKFSFGQCIDCASGTF 120
QY 121 SGHEGHCKPWTDTCTQFGLTVFPGKNTNANVCVPGSPPAEPGLGWLTVLLVAACVLL 180
Db 121 SGHEGHCKPWTDTCTQFGLTVFPGKNTNANVCVPGSPPAEPGLGWLTVLLVAACVLL 180
QY 181 TSAQLGLHIWQLRSQCMWPRETQLLEVPSTEDARSCQPFPEERGERSAEKGRLGLDW 240
Db 181 TSAQLGLHIWQLRSQCMWPRETQLLEVPSTEDARSCQPFPEERGERSAEKGRLGLDW 240
QY 241 V 241
Db 241 V 241
RESULT 15
ABU08442
ID ABU08442 standard; protein; 241 AA.
XX

AC ABU08442;
XX 13-JUN-2003 (first entry)
XX Amino acid sequence for human TR11 polypeptide.
DE Human; tumour necrosis factor receptor family; TNF receptor; TR11;
KW endokine-alpha; endokine-alpha receptor; immunodeficiency disease;
KW severe combined immunodeficiency-X linked; SCID-X linked; SLE;
KW Bruton's disease; dysgammaglobulinaemia; autoimmune disease;
KW systemic lupus erythematosus; rheumatoid arthritis; dermatitis;
KW allergic encephalomyelitis; immunostimulant; dermatological;
KW immunosuppressive; antiinflammatory; antirheumatic; antiarthritic;
KW antiallergic.
XX Homo sapiens.
OS US6503184-B1.
XX 07-JAN-2003.
XX 23-FEB-2000; 2000US-00512363.
XX 21-OCT-1997; 97US-0063212P.
XX 21-OCT-1998; 98US-00176200.
XX 24-FEB-1999; 99US-0121648P.
XX 13-MAY-1999; 99US-0134172P.
XX 16-JUL-1999; 99US-0144076P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Ni J, Ruben SM;
XX WPI; 2003-352213/33.
XX Inhibiting binding of endokine-alpha to endogenous endokine-alpha
PT receptors in a mammal, by administering to a mammal a fragment of human
PT tumor necrosis factor receptor-related protein.
XX Disclosure; Col 201-202; 114pp; English.
XX The present invention relates to the isolation of novel members of the
CC tumour necrosis factor (TNF) family of receptors, referred to as TNF
CC receptor-related proteins and designated TR11, TR11SV1 and TR11SV2.
CC TR11SV1 and TR11SV2 represent splice variants of TR11. The invention also
CC discloses the polynucleotide sequences encoding the TR11 receptors, and a
CC method of inhibiting endokine-alpha binding to endogenous endokine-alpha
CC receptors in mammals. The method of the invention is useful for
CC inhibiting the binding of endokine-alpha to endogenous endokine-alpha
CC receptors in a mammal, preferably humans. The method is useful for
CC treating or preventing immunodeficiency diseases (e.g. severe combined
CC immunodeficiency (SCID)-X linked, Bruton's disease,
CC dysgammaglobulinaemia), and autoimmune diseases (e.g. systemic lupus
CC erythematosus (SLE), rheumatoid arthritis, dermatitis, allergic
CC encephalomyelitis). The present sequence represents human TR11
XX polypeptide
SQ Sequence 241 AA;

Query Match 100.0%; Score 1386; DB 6; Length 241;
Best Local Similarity 100.0%; Pred. No. 2.2e-101;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHGMAGAFRALCGLALLCALSLGQRTGGPGCGPGRLLLTGTGTDCRCRVHTTRCCRD 60
DB 1 MAQHGMAGAFRALCGLALLCALSLGQRTGGPGCGPGRLLLTGTGTDCRCRVHTTRCCRD 60
QY 61 YPGEECCSWDCMCVQPEPHCGDPCTTCRHHPCPPGQGVQSGKFSFGFCIDCASGTF 120
DB 61 YPGEECCSEWDCMCVQPEPHCGDPCTTCRHHPCPPGQGVQSGKFSFGFCIDCASGTF 120
QY 121 SGGHEGHCCKPWTCTQFGFLTVPFGNKTNAVCPGSPPAEPLGWLTVVLLAAVACVLLL 180

Db 121 SGGHEGHCCKPWTCTQFGFLTVPFGNKTNAVCPGSPPAEPLGWLTVVLLAAVACVLLL 180
QY 181 TSAQLGLHIWQLRSQCMWPRETQLLLLEVPPTEDARSQCFPEERGERSABEKGLGLIW 240
Db 181 TSAQLGLHIWQLRSQCMWPRETQLLLLEVPPTEDARSQCFPEERGERSABEKGLGLIW 240
QY 241 V 241
Db 241 V 241
Search completed: October 26, 2005, 15:47:40
Job time : 142.311 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 26, 2005, 15:51:55 ; Search time 115.618 Seconds
(without alignments)
870.278 Million cell updates/sec

Title: US-09-545-998B-4
Perfect score: 1386
Sequence: 1 MAQHAGMAGFRALCGLALIC.....EEGERSAEEKGRGLDLWV 241

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1862994 seqs, 417510619 residues

Total number of hits satisfying chosen parameters: 1862994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10F_PUBCOMB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US10G_PUBCOMB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US10H_PUBCOMB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1386	100.0	241	9 US-09-915-593-28	Sequence 28, Appl
2	1386	100.0	241	13 US-10-116-378-3	Sequence 3, Appli
3	1386	100.0	241	14 US-10-283-105-28	Sequence 28, Appl
4	1386	100.0	241	14 US-10-277-966-28	Sequence 28, Appl
5	1386	100.0	241	15 US-10-295-027-1284	Sequence 1284, Ap
6	1386	100.0	241	17 US-10-959-537-3	Sequence 3, Appli
7	1386	100.0	241	20 US-11-032-294-3	Sequence 3, Appli
8	1382	99.7	240	16 US-10-783-528-75	Sequence 75, Appl
9	1322.5	95.4	234	9 US-09-915-593-2	Sequence 2, Appli
10	1322.5	95.4	234	14 US-10-283-105-2	Sequence 2, Appli
11	1322.5	95.4	234	14 US-10-277-966-2	Sequence 2, Appli

12	1306.5	94.3	246	15 US-10-264-237-1762	Sequence 1762, Ap
13	1274.5	92.0	240	9 US-09-915-593-6	Sequence 6, Appli
14	1274.5	92.0	240	14 US-10-283-105-6	Sequence 6, Appli
15	1274.5	92.0	240	14 US-10-277-966-6	Sequence 6, Appli
16	1056	76.2	241	9 US-09-915-593-4	Sequence 4, Appli
17	1056	76.2	241	14 US-10-283-105-4	Sequence 4, Appli
18	1056	76.2	241	14 US-10-277-966-4	Sequence 4, Appli
19	953	68.8	317	13 US-10-116-378-26	Sequence 26, Appl
20	953	68.8	317	17 US-10-959-537-26	Sequence 26, Appl
21	735.5	53.1	228	9 US-09-915-593-7	Sequence 7, Appli
22	735.5	53.1	228	13 US-10-116-378-24	Sequence 24, Appl
23	735.5	53.1	228	14 US-10-283-105-7	Sequence 7, Appli
24	735.5	53.1	228	14 US-10-277-966-7	Sequence 7, Appli
25	735.5	53.1	228	17 US-10-959-537-24	Sequence 24, Appl
26	255	18.4	89	10 US-09-866-050A-191	Sequence 191, App
27	201.5	14.5	276	15 US-10-369-300-4	Sequence 4, Appli
28	197	14.2	256	13 US-10-027-199-10	Sequence 10, Appl
29	197	14.2	256	14 US-10-067-122-2	Sequence 2, Appli
30	197	14.2	256	17 US-10-981-352-4	Sequence 4, Appli
31	195.5	14.1	255	9 US-09-739-394-9	Sequence 9, Appli
32	195.5	14.1	255	9 US-09-826-213-11	Sequence 11, Appl
33	195.5	14.1	255	9 US-09-935-727-13	Sequence 13, Appl
34	195.5	14.1	255	10 US-09-877-336-2	Sequence 2, Appli
35	195.5	14.1	255	11 US-09-877-338-2	Sequence 2, Appli
36	195.5	14.1	255	13 US-10-097-330-9	Sequence 9, Appli
37	195.5	14.1	255	13 US-10-027-199-2	Sequence 2, Appli
38	195.5	14.1	255	14 US-10-170-997-2	Sequence 2, Appli
39	195.5	14.1	255	14 US-10-186-643-11	Sequence 11, Appl
40	195.5	14.1	255	14 US-10-207-655-160	Sequence 160, App
41	195.5	14.1	255	15 US-10-418-242-13	Sequence 13, Appl
42	195.5	14.1	255	16 US-10-646-308-18	Sequence 18, Appl
43	195.5	14.1	255	16 US-10-755-889-174	Sequence 174, App
44	195.5	14.1	255	16 US-10-748-112-15	Sequence 15, Appl
45	195.5	14.1	255	16 US-10-723-860-588	Sequence 588, App

ALIGNMENTS

RESULT 1
US-09-915-593-28
; Sequence 28, Application US/09915593
; Patent No. US20020098525A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins
; TITLE OF INVENTION: TR11, TR11SV1, and TR11SV2
; FILE REFERENCE: PF396P2
; CURRENT APPLICATION NUMBER: US/09/915,593
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/221,577
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 09/512,363
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/144,076
; PRIOR FILING DATE: 2000-07-16
; PRIOR APPLICATION NUMBER: 60/134,172
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: 60/121,648
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 09/176,200
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/063,212
; PRIOR FILING DATE: 1997-10-21
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 28
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-915-593-28

Query Match 100.0%; Score 1386; DB 9; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.1e-106;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHGMGAFRALCGLALLCALSLGQRTGGPGCGPGRLLLTGTDTARCCRVHTTRCCRD 60
DB 1 MAQHGMGAFRALCGLALLCALSLGQRTGGPGCGPGRLLLTGTDTARCCRVHTTRCCRD 60

QY 61 YPGECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSGKPSFGFCIDCASGTF 120
DB 61 YPGECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSGKPSFGFCIDCASGTF 120

QY 121 SGHGHGCKPWTDCQFGFLTVPPGNKTHNAVCPGSPPAEPLGMLTVVLLAAVACVLL 180
DB 121 SGHGHGCKPWTDCQFGFLTVPPGNKTHNAVCPGSPPAEPLGMLTVVLLAAVACVLL 180

QY 181 TSAQLGLHIWQLRSQCMWPRETQLLEVPSTEDARSCQFPPEERGERSAEKGRIGDLW 240
DB 181 TSAQLGLHIWQLRSQCMWPRETQLLEVPSTEDARSCQFPPEERGERSAEKGRIGDLW 240

QY 241 V 241
DB 241 V 241

RESULT 2
US-10-116-378-3
; Sequence 3, Application US/10116378
; Publication No. US20020150993A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pitti, Robert M.
; APPLICANT: Wood, William
; TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOG AND
; TITLE OF INVENTION: NUCLEIC
; FILE REFERENCE: ACIDS ENCODING THE SAME
; CURRENT APPLICATION NUMBER: US/10/116,378
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/247,225
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/074,087
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-09
; NUMBER OF SEQ ID NOS: 31
; SEQ ID NO 3
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-116-378-3

Query Match 100.0%; Score 1386; DB 13; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.1e-106;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHGMGAFRALCGLALLCALSLGQRTGGPGCGPGRLLLTGTDTARCCRVHTTRCCRD 60
DB 1 MAQHGMGAFRALCGLALLCALSLGQRTGGPGCGPGRLLLTGTDTARCCRVHTTRCCRD 60

QY 61 YPGECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSGKPSFGFCIDCASGTF 120
DB 61 YPGECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSGKPSFGFCIDCASGTF 120

QY 121 SGHGHGCKPWTDCQFGFLTVPPGNKTHNAVCPGSPPAEPLGMLTVVLLAAVACVLL 180
DB 121 SGHGHGCKPWTDCQFGFLTVPPGNKTHNAVCPGSPPAEPLGMLTVVLLAAVACVLL 180

QY 181 TSAQLGLHIWQLRSQCMWPRETQLLEVPSTEDARSCQFPPEERGERSAEKGRIGDLW 240
DB 181 TSAQLGLHIWQLRSQCMWPRETQLLEVPSTEDARSCQFPPEERGERSAEKGRIGDLW 240

QY 241 V 241
DB 241 V 241

RESULT 3
US-10-283-105-28
; Sequence 28, Application US/10283105
; Publication No. US20030138426A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Ruben, Steven M
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins TR11, TR11SV1,
; TITLE OF INVENTION: TR11SV22
; FILE REFERENCE: PF396P3
; CURRENT APPLICATION NUMBER: US/10/283,105
; PRIOR FILING DATE: 2002-10-30
; PRIOR APPLICATION NUMBER: 60/330,757
; PRIOR FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 09/915,593
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/221,577
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 09/512,363
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/144,076
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 60/134,172
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: 60/121,648
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 09/176,200
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/063,212
; PRIOR FILING DATE: 1997-10-21
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 241
; TYPE: PRT
; ORGANISM: human
US-10-283-105-28

Query Match 100.0%; Score 1386; DB 14; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.1e-106;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHGMGAFRALCGLALLCALSLGQRTGGPGCGPGRLLLTGTDTARCCRVHTTRCCRD 60
DB 1 MAQHGMGAFRALCGLALLCALSLGQRTGGPGCGPGRLLLTGTDTARCCRVHTTRCCRD 60

QY 61 YPGECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSGKPSFGFCIDCASGTF 120
DB 61 YPGECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSGKPSFGFCIDCASGTF 120

QY 121 SGHGHGCKPWTDCQFGFLTVPPGNKTHNAVCPGSPPAEPLGMLTVVLLAAVACVLL 180
DB 121 SGHGHGCKPWTDCQFGFLTVPPGNKTHNAVCPGSPPAEPLGMLTVVLLAAVACVLL 180

QY 181 TSAQLGLHIWQLRSQCMWPRETQLLEVPSTEDARSCQFPPEERGERSAEKGRIGDLW 240
DB 181 TSAQLGLHIWQLRSQCMWPRETQLLEVPSTEDARSCQFPPEERGERSAEKGRIGDLW 240

QY 241 V 241
DB 241 V 241

RESULT 4
US-10-277-966-28
; Sequence 28, Application US/10277966
; Publication No. US20030153499A1
; GENERAL INFORMATION:

APPLICANT: Ni, Jian
APPLICANT: Ruben, Steven
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins TR11, TR11SV1,
FILE REFERENCE: PF396PDI1
CURRENT APPLICATION NUMBER: US/10/277,966
CURRENT FILING DATE: 2002-10-23
PRIOR APPLICATION NUMBER: 09/512,363
PRIOR FILING DATE: 2000-02-23
PRIOR APPLICATION NUMBER: 60/121,648
PRIOR FILING DATE: 1999-02-24
PRIOR APPLICATION NUMBER: 60/134,172
PRIOR FILING DATE: 1999-05-13
PRIOR APPLICATION NUMBER: 60/144,076
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: 09/176,200
PRIOR FILING DATE: 1998-10-21
PRIOR APPLICATION NUMBER: 60/063,212
PRIOR FILING DATE: 1997-10-21
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.1
SEQ ID NO 28
LENGTH: 241
TYPE: PRT
ORGANISM: human
US-10-277-966-28

Query Match 100.0%; Score 1386; DB 14; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.1e-106;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHGAMGAFRALCGALLCALSLGQRTGCGGCGPGRLLLTGTDAARCCRVHTTRCCRD 60
DB 1 MAQHGAMGAFRALCGALLCALSLGQRTGCGGCGPGRLLLTGTDAARCCRVHTTRCCRD 60

QY 61 YPGECCSEWDMCMVQPEFHCGDPCCCTTCRHHPCPPGQGVQSGQKFSFGQCIDCASGTF 120
DB 61 YPGECCSEWDMCMVQPEFHCGDPCCCTTCRHHPCPPGQGVQSGQKFSFGQCIDCASGTF 120

QY 121 SGHGHGCKPWTCTQGFGLTVFPGNKNTHNAVCPGSPPAEPLGWLTVLLVAACVLLL 180
DB 121 SGHGHGCKPWTCTQGFGLTVFPGNKNTHNAVCPGSPPAEPLGWLTVLLVAACVLLL 180

QY 181 TSAQLGHIWQLRSQCMWPRETQLLLEVPSTEDARSCQPEEERGSAAEKGRLGDLW 240
DB 181 TSAQLGHIWQLRSQCMWPRETQLLLEVPSTEDARSCQPEEERGSAAEKGRLGDLW 240

QY 241 V 241
DB 241 V 241

RESULT 5
US-10-295-027-1284
Sequence 1284, Application US/10295027
Publication No. US20030232350A1
GENERAL INFORMATION:
APPLICANT: Afar, Daniel
APPLICANT: Aziz, Natasha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Gish, Kurt C.
APPLICANT: Glynn, Richard
APPLICANT: Hevezi, Peter A.
APPLICANT: Mack, David H.
APPLICANT: Murray, Richard
APPLICANT: Watson, Susan R.
APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of diagnosis of Cancer, Compositions and
METHODS OF INVENTION: Methods of Screening for Modulators of Cancer
FILE REFERENCE: 018501-012500US
CURRENT APPLICATION NUMBER: US/10/295,027
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: US 09/663,733

PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/335,394
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: US 60/334,393
PRIOR FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: US 60/340,376
PRIOR FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: US 60/347,211
PRIOR FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US 60/347,349
PRIOR FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 60/355,250
PRIOR FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US 60/356,714
PRIOR FILING DATE: 2002-02-13
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1386
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1284
LENGTH: 241
TYPE: PRT
ORGANISM: Homo sapiens
US-10-295-027-1284

Query Match 100.0%; Score 1386; DB 15; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.1e-106;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQHGAMGAFRALCGALLCALSLGQRTGCGGCGPGRLLLTGTDAARCCRVHTTRCCRD 60
DB 1 MAQHGAMGAFRALCGALLCALSLGQRTGCGGCGPGRLLLTGTDAARCCRVHTTRCCRD 60

QY 61 YPGECCSEWDMCMVQPEFHCGDPCCCTTCRHHPCPPGQGVQSGQKFSFGQCIDCASGTF 120
DB 61 YPGECCSEWDMCMVQPEFHCGDPCCCTTCRHHPCPPGQGVQSGQKFSFGQCIDCASGTF 120

QY 121 SGHGHGCKPWTCTQGFGLTVFPGNKNTHNAVCPGSPPAEPLGWLTVLLVAACVLLL 180
DB 121 SGHGHGCKPWTCTQGFGLTVFPGNKNTHNAVCPGSPPAEPLGWLTVLLVAACVLLL 180

QY 181 TSAQLGHIWQLRSQCMWPRETQLLLEVPSTEDARSCQPEEERGSAAEKGRLGDLW 240
DB 181 TSAQLGHIWQLRSQCMWPRETQLLLEVPSTEDARSCQPEEERGSAAEKGRLGDLW 240

QY 241 V 241
DB 241 V 241

RESULT 6
US-10-959-537-3
Sequence 3, Application US/10959537
Publication No. US20050069983A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin
APPLICANT: Marsters, Scot A.
APPLICANT: Pitti, Robert M.
APPLICANT: Wood, William
TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOG AND NUCLEIC
ACIDS ENCODING THE SAME
FILE REFERENCE: P1206R1
CURRENT APPLICATION NUMBER: US/10/959,537
CURRENT FILING DATE: 2004-10-06
PRIOR APPLICATION NUMBER: US/09/247,225
PRIOR FILING DATE: 1999-02-09
PRIOR APPLICATION NUMBER: US 60/074,087
PRIOR FILING DATE: 1998-02-09

```
; NUMBER OF SEQ ID NOS: 31
; SEQ ID NO 3
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-959-537-3

Query Match      100.0%; Score 1386; DB 17; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.1e-106;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAOHGAMGAFRALCGLLALLCALSLGQRTGPGCGPGRLLLTGTDTARCCRVHTTRCCRD 60
DB 1 MAOHGAMGAFRALCGLLALLCALSLGQRTGPGCGPGRLLLTGTDTARCCRVHTTRCCRD 60

QY 61 YPGECCSSEWDCMCVQPEPHCGDPCCCTTCRHHPCPPGQVQSGKFSFGFCIDCASGTF 120
DB 61 YPGECCSSEWDCMCVQPEPHCGDPCCCTTCRHHPCPPGQVQSGKFSFGFCIDCASGTF 120

QY 121 SGHGHGCHKPWTDCQFGFLTVPFGNKTNAVCVPGSPPAEPLGMLTVVLLAAVACVLL 180
DB 121 SGHGHGCHKPWTDCQFGFLTVPFGNKTNAVCVPGSPPAEPLGMLTVVLLAAVACVLL 180

QY 181 TSAQLGLHIWQLRSQCMWPRETQLLLEVPSTEDARSCQFPPEERGERSAEEKGRGLD 240
DB 181 TSAQLGLHIWQLRSQCMWPRETQLLLEVPSTEDARSCQFPPEERGERSAEEKGRGLD 240

QY 241 V 241
DB 241 V 241

Query Match      99.7%; Score 1382; DB 16; Length 240;
Best Local Similarity 100.0%; Pred. No. 2.4e-106;
Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAOHGAMGAFRALCGLLALLCALSLGQRTGPGCGPGRLLLTGTDTARCCRVHTTRCCRD 60
DB 1 MAOHGAMGAFRALCGLLALLCALSLGQRTGPGCGPGRLLLTGTDTARCCRVHTTRCCRD 60

QY 61 YPGECCSSEWDCMCVQPEPHCGDPCCCTTCRHHPCPPGQVQSGKFSFGFCIDCASGTF 120
DB 61 YPGECCSSEWDCMCVQPEPHCGDPCCCTTCRHHPCPPGQVQSGKFSFGFCIDCASGTF 120

QY 121 SGHGHGCHKPWTDCQFGFLTVPFGNKTNAVCVPGSPPAEPLGMLTVVLLAAVACVLL 180
DB 121 SGHGHGCHKPWTDCQFGFLTVPFGNKTNAVCVPGSPPAEPLGMLTVVLLAAVACVLL 180

QY 181 TSAQLGLHIWQLRSQCMWPRETQLLLEVPSTEDARSCQFPPEERGERSAEEKGRGLD 240
DB 181 TSAQLGLHIWQLRSQCMWPRETQLLLEVPSTEDARSCQFPPEERGERSAEEKGRGLD 240

RESULT 9
US-09-915-593-2
; Sequence 2, Application US/09915593
; Patent No. US20020098525A1
; GENERAL INFORMATION:
; APPLICANT: NI, Jian
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins
; TITLE OF INVENTION: TR11, TR11SV1, and TR11SV2
; FILE REFERENCE: PF396P2
; CURRENT APPLICATION NUMBER: US/09/915,593
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/221,577
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 09/512,363
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/144,076
; PRIOR FILING DATE: 2000-07-16
; PRIOR APPLICATION NUMBER: 60/134,172
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: 60/121,648
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 09/176,200

; NUMBER OF SEQ ID NOS: 31
; SEQ ID NO 3
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-959-537-3

Query Match      100.0%; Score 1386; DB 20; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.1e-106;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAOHGAMGAFRALCGLLALLCALSLGQRTGPGCGPGRLLLTGTDTARCCRVHTTRCCRD 60
DB 1 MAOHGAMGAFRALCGLLALLCALSLGQRTGPGCGPGRLLLTGTDTARCCRVHTTRCCRD 60

QY 61 YPGECCSSEWDCMCVQPEPHCGDPCCCTTCRHHPCPPGQVQSGKFSFGFCIDCASGTF 120
DB 61 YPGECCSSEWDCMCVQPEPHCGDPCCCTTCRHHPCPPGQVQSGKFSFGFCIDCASGTF 120

QY 121 SGHGHGCHKPWTDCQFGFLTVPFGNKTNAVCVPGSPPAEPLGMLTVVLLAAVACVLL 180
DB 121 SGHGHGCHKPWTDCQFGFLTVPFGNKTNAVCVPGSPPAEPLGMLTVVLLAAVACVLL 180

QY 181 TSAQLGLHIWQLRSQCMWPRETQLLLEVPSTEDARSCQFPPEERGERSAEEKGRGLD 240
DB 181 TSAQLGLHIWQLRSQCMWPRETQLLLEVPSTEDARSCQFPPEERGERSAEEKGRGLD 240

US-11-032-294-3
; Sequence 3, Application US/11032294
; Publication No. US20050202008A1
; GENERAL INFORMATION:
; APPLICANT: P. Mickey Williams
; APPLICANT: Mary E. Gerritsen
; TITLE OF INVENTION: PROMOTION OR INHIBITION OF ANGIOGENESIS AND
; TITLE OF INVENTION: CARDIOVASCULARIZATION BY TUMOR NECROSIS FACTOR
; TITLE OF INVENTION: LIGAND/RECEPTOR HOMOLOGS
; FILE REFERENCE: PI765R1
; CURRENT APPLICATION NUMBER: US/11/032,294
; CURRENT FILING DATE: 2005-01-10
; PRIOR APPLICATION NUMBER: CURRENT FILING DATE: 2000-07-11
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: US 60/143,304
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 22
; SEQ ID NO 3
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-032-294-3

Query Match      100.0%; Score 1386; DB 20; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.1e-106;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAOHGAMGAFRALCGLLALLCALSLGQRTGPGCGPGRLLLTGTDTARCCRVHTTRCCRD 60
DB 1 MAOHGAMGAFRALCGLLALLCALSLGQRTGPGCGPGRLLLTGTDTARCCRVHTTRCCRD 60

QY 61 YPGECCSSEWDCMCVQPEPHCGDPCCCTTCRHHPCPPGQVQSGKFSFGFCIDCASGTF 120
DB 61 YPGECCSSEWDCMCVQPEPHCGDPCCCTTCRHHPCPPGQVQSGKFSFGFCIDCASGTF 120

QY 121 SGHGHGCHKPWTDCQFGFLTVPFGNKTNAVCVPGSPPAEPLGMLTVVLLAAVACVLL 180
DB 121 SGHGHGCHKPWTDCQFGFLTVPFGNKTNAVCVPGSPPAEPLGMLTVVLLAAVACVLL 180

QY 181 TSAQLGLHIWQLRSQCMWPRETQLLLEVPSTEDARSCQFPPEERGERSAEEKGRGLD 240
DB 181 TSAQLGLHIWQLRSQCMWPRETQLLLEVPSTEDARSCQFPPEERGERSAEEKGRGLD 240
```

; PRIOR FILING DATE: 1998-10-21
 ; PRIOR APPLICATION NUMBER: 60/063,212
 ; PRIOR FILING DATE: 1997-10-21
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 234
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-545-998b-4

Query Match 95.4%; Score 1322.5; DB 9; Length 234;
 Best Local Similarity 96.7%; Pred. No. 1.9e-101;
 Matches 233; Conservative 1; Mismatches 0; Indels 7; Gaps 1;
 QY 1 MAQHGAMGAFRALCGLLALCALSLGQRTGPGCGGPRLLLTGTDAARCRVHTTRCCRD 60
 DB 1 MAQHGAMGAFRALCGLLALCALSLGQRTGPGCGGPRLLLTGTDAARCRVHTTRCCRD 60
 QY 61 YPGECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFCIDCASGTF 120
 DB 61 YPGECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFCIDCASGTF 120
 QY 121 SGGHEGCHKPWTDTCTQFGFLTVPFGNKTNAVCVPGSPPAEPGLGWLTVVLLAVAAACVLLL 180
 DB 121 SGGHEGCHKPWTDTCTQFGFLTVPFGNKTNAVCVPGSPPAEPGLGWLTVVLLAVAAACVLLL 180
 QY 181 TSAQLGLHIWQLRSQCMWPRETQLLEVPSTEDARSCQPPPEERGERSAEEKRGLDGLW 240
 DB 181 TSAQLGLHIWQLRSQCMWPRETQLLEVPSTEDARSCQPPPEERGERSAEEKRGLDGLW 240
 QY 241 V 241
 DB 234 V 234

RESULT 10
 US-10-283-105-2
 ; Sequence 2, Application US/10283105
 ; Publication No. US20030138426A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ni, Jian
 ; APPLICANT: Ruben, Steven M
 ; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins TR11, TR11SV1,
 ; FILE REFERENCE: PF396P3
 ; CURRENT APPLICATION NUMBER: US/10283,105
 ; PRIOR FILING DATE: 2002-10-30
 ; PRIOR APPLICATION NUMBER: 60/330,757
 ; PRIOR FILING DATE: 2001-10-30
 ; PRIOR APPLICATION NUMBER: 60/915,593
 ; PRIOR FILING DATE: 2001-07-27
 ; PRIOR APPLICATION NUMBER: 60/221,577
 ; PRIOR FILING DATE: 2000-07-28
 ; PRIOR APPLICATION NUMBER: 09/512,363
 ; PRIOR FILING DATE: 2000-02-23
 ; PRIOR APPLICATION NUMBER: 60/144,076
 ; PRIOR FILING DATE: 1999-07-16
 ; PRIOR APPLICATION NUMBER: 60/134,172
 ; PRIOR FILING DATE: 1999-05-13
 ; PRIOR APPLICATION NUMBER: 60/121,648
 ; PRIOR FILING DATE: 1999-02-24
 ; PRIOR APPLICATION NUMBER: 09/176,200
 ; PRIOR FILING DATE: 1998-10-21
 ; PRIOR APPLICATION NUMBER: 60/063,212
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 2
 ; LENGTH: 234
 ; TYPE: PRT
 ; ORGANISM: human
 ; US-10-283-105-2

Query Match 95.4%; Score 1322.5; DB 14; Length 234;
 Best Local Similarity 96.7%; Pred. No. 1.9e-101;
 Matches 233; Conservative 1; Mismatches 0; Indels 7; Gaps 1;
 QY 1 MAQHGAMGAFRALCGLLALCALSLGQRTGPGCGGPRLLLTGTDAARCRVHTTRCCRD 60
 DB 1 MAQHGAMGAFRALCGLLALCALSLGQRTGPGCGGPRLLLTGTDAARCRVHTTRCCRD 60
 QY 61 YPGECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFCIDCASGTF 120
 DB 61 YPGECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFCIDCASGTF 120
 QY 121 SGGHEGCHKPWTDTCTQFGFLTVPFGNKTNAVCVPGSPPAEPGLGWLTVVLLAVAAACVLLL 180
 DB 121 SGGHEGCHKPWTDTCTQFGFLTVPFGNKTNAVCVPGSPPAEPGLGWLTVVLLAVAAACVLLL 180
 QY 181 TSAQLGLHIWQLRSQCMWPRETQLLEVPSTEDARSCQPPPEERGERSAEEKRGLDGLW 240
 DB 181 TSAQLGLHIWQLRSQCMWPRETQLLEVPSTEDARSCQPPPEERGERSAEEKRGLDGLW 240
 QY 241 V 241
 DB 234 V 234

RESULT 11
 US-10-277-966-2
 ; Sequence 2, Application US/10277966
 ; Publication No. US20030153499A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ni, Jian
 ; APPLICANT: Ruben, Steven
 ; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins TR11, TR11SV1,
 ; FILE REFERENCE: PF396PDI
 ; CURRENT APPLICATION NUMBER: US/10277,966
 ; PRIOR FILING DATE: 2002-10-23
 ; PRIOR APPLICATION NUMBER: 09/512,363
 ; PRIOR FILING DATE: 2000-02-23
 ; PRIOR APPLICATION NUMBER: 60/121,648
 ; PRIOR FILING DATE: 1999-02-24
 ; PRIOR APPLICATION NUMBER: 60/134,172
 ; PRIOR FILING DATE: 1999-05-13
 ; PRIOR APPLICATION NUMBER: 60/144,076
 ; PRIOR FILING DATE: 1999-07-16
 ; PRIOR APPLICATION NUMBER: 09/176,200
 ; PRIOR FILING DATE: 1998-10-21
 ; PRIOR APPLICATION NUMBER: 60/063,212
 ; PRIOR FILING DATE: 1997-10-21
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 2
 ; LENGTH: 234
 ; TYPE: PRT
 ; ORGANISM: human
 ; US-10-277-966-2

Query Match 95.4%; Score 1322.5; DB 14; Length 234;
 Best Local Similarity 96.7%; Pred. No. 1.9e-101;
 Matches 233; Conservative 1; Mismatches 0; Indels 7; Gaps 1;
 QY 1 MAQHGAMGAFRALCGLLALCALSLGQRTGPGCGGPRLLLTGTDAARCRVHTTRCCRD 60
 DB 1 MAQHGAMGAFRALCGLLALCALSLGQRTGPGCGGPRLLLTGTDAARCRVHTTRCCRD 60
 QY 61 YPGECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFCIDCASGTF 120
 DB 61 YPGECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFCIDCASGTF 120
 QY 121 SGGHEGCHKPWTDTCTQFGFLTVPFGNKTNAVCVPGSPPAEPGLGWLTVVLLAVAAACVLLL 180
 DB 121 SGGHEGCHKPWTDTCTQFGFLTVPFGNKTNAVCVPGSPPAEPGLGWLTVVLLAVAAACVLLL 180

```
QY 181 TSAQLGLHQLWRSQCMWPRETQLLEVPSTEDARSCQFPPEERGSABEKRLGLDW 240
Db 181 TSAQLGLHQLW-----RKTQLLEVPSTEDARSCQFPPEERGSABEKRLGLDW 233
QY 241 V 241
Db 234 V 234

RESULT 12
US-10-264-237-1762
; Sequence 1762, Application US/10264237
; Publication No. US2004009491A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 1762
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-237-1762

Query Match 94.3%; Score 1306.5; DB 15; Length 246;
Best Local Similarity 92.1%; Pred. No. 4.3e-100;
Matches 233; Conservative 1; Mismatches 0; Indels 19; Gaps 2;

QY 1 MAQHGAMGAFRALCGLALCALSLGQRTGGPGCGPRLLLGTGTDAACRCRVHTTRCCRD 60
Db 1 MAQHGAMGAFRALCGLALCALSLGQRTGGPGCGPRLLLGTGTDAACRCRVHTTRCCRD 60
QY 61 Y-----PGECCSEWDCMCVQPEFHCQDPCCCTTCTRHHPCPGQGVQSGKFSF 108
Db 61 YPAQLLGGHVPVSCFGECCSEWDCMCVQPEFHCQDPCCCTTCTRHHPCPGQGVQSGKFSF 120
QY 109 GFQCIDCASGTFSGGHEGCHKPWTCTQFGFLTVPFGKNTNACVCPGPPAEPLGWLTV 168
Db 121 GFQCIDCASGTFSGGHEGCHKPWTCTQFGFLTVPFGKNTNACVCPGPPAEPLGWLTV 180
QY 169 VLLAVAACVLLLTSAQLGLHQLWRSQCMWPRETQLLEVPSTEDARSCQFPPEERGER 228
Db 181 VLLAVAACVLLLTSAQLGLHQLW-----RKTQLLEVPSTEDARSCQFPPEERGER 233
QY 229 SAEKGRGLGLW 241
Db 234 SAEKGRGLGLW 246

RESULT 13
US-09-915-593-6
; Sequence 6, Application US/09915593
; Patent No. US20020098525A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins
; TITLE OF INVENTION: TR11, TR11SV1, and TR11SV2
; FILE REFERENCE: PF396P2
; CURRENT APPLICATION NUMBER: US/09/915,593
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/221,577
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 09/512,363
; PRIOR FILING DATE: 2000-02-23
```

```
; PRIOR APPLICATION NUMBER: 60/144,076
; PRIOR FILING DATE: 2000-07-16
; PRIOR APPLICATION NUMBER: 60/134,172
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: 60/121,648
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 09/176,200
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/063,212
; PRIOR FILING DATE: 1997-10-21
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-593-6

Query Match 92.0%; Score 1274.5; DB 9; Length 240;
Best Local Similarity 91.9%; Pred. No. 1.9e-97;
Matches 227; Conservative 1; Mismatches 0; Indels 19; Gaps 2;

QY 7 MGAFFRALCGLALCALSLGQRTGGPGCGPRLLLGTGTDAACRCRVHTTRCCRDY----- 61
Db 1 MGAFFRALCGLALCALSLGQRTGGPGCGPRLLLGTGTDAACRCRVHTTRCCRDYPAQLL 60
QY 62 -----PGECCSEWDCMCVQPEFHCQDPCCCTTCTRHHPCPGQGVQSGKFSFGQCID 114
Db 61 GGWPVSCFGECCSEWDCMCVQPEFHCQDPCCCTTCTRHHPCPGQGVQSGKFSFGQCID 120
QY 115 CASGTFSGGHEGCHKPWTCTQFGFLTVPFGKNTNACVCPGPPAEPLGWLTVVLLAVA 174
Db 121 CASGTFSGGHEGCHKPWTCTQFGFLTVPFGKNTNACVCPGPPAEPLGWLTVVLLAVA 180
QY 175 ACVLLLTSAQLGLHQLWRSQCMWPRETQLLEVPSTEDARSCQFPPEERGSABEKG 234
Db 181 ACVLLLTSAQLGLHQLW-----RKTQLLEVPSTEDARSCQFPPEERGSABEKG 233
QY 235 RLGLDLW 241
Db 234 RLGLDLW 240

RESULT 14
US-10-283-105-6
; Sequence 6, Application US/10283105
; Publication No. US20030138426A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Ruben, Steven M
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins TR11, TR11SV1,
; TITLE OF INVENTION: TR11SV2
; FILE REFERENCE: PF396P3
; CURRENT APPLICATION NUMBER: US/10/283,105
; CURRENT FILING DATE: 2002-10-30
; PRIOR APPLICATION NUMBER: 60/330,757
; PRIOR FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 09/915,593
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/221,577
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 09/512,363
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/144,076
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 60/134,172
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: 60/121,648
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 09/176,200
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/063,212
; PRIOR FILING DATE: 1997-10-21
```



```

; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 240
; TYPE: PRT
; ORGANISM: human
US-10-283-105-6

Query Match          92.0%; Score 1274.5; DB 14; Length 240;
Best Local Similarity 91.9%; Pred. No. 1.9e-97;
Matches 227; Conservative 1; Mismatches 0; Indels 19; Gaps 2;

QY 7 MGAFRALCGLLALCALSLGQRTGGPGCGPGRLLLTGTGDARCRVHTTRCCRDY----- 61
DB 1 MGAFRALCGLLALCALSLGQRTGGPGCGPGRLLLTGTGDARCRVHTTRCCRDYPAQLL 60

QY 62 -----PGECCSEWDCMCVQPEFHGCDPCCTTCRRHPCPPGQGVQSQGKFSFGQCID 114
DB 61 GGPVSPGPECCSEWDCMCVQPEFHGCDPCCTTCRRHPCPPGQGVQSQGKFSFGQCID 120

QY 115 CASGTFSGGHEGHCCKPWTDTCTQFGFLTVPFGNKNTHNAVCPGSPPAEPLGMLTVVLLAVA 174
DB 121 CASGTFSGGHEGHCCKPWTDTCTQFGFLTVPFGNKNTHNAVCPGSPPAEPLGMLTVVLLAVA 180

QY 175 ACVLLLTSAQLGLHIWQLRSQCMWMPRETQLLLEVPPTSTEDARSCQFPEERGERGSAEEKG 234
DB 181 ACVLLLTSAQLGLHIWQL-----RKTQLLLEVPPTSTEDARSCQFPEERGERGSAEEKG 233

QY 235 RLGDLMV 241
DB 234 RLGDLMV 240

Search completed: October 26, 2005, 16:11:21
Job time : 116.618 secs
```

```

RESULT 15
US-10-277-966-6
; Sequence 6, Application US/10277966
; Publication No. US20030153499A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins Tr11, Tr11SV1,
; TITLE OF INVENTION: Tr11SV2
; FILE REFERENCE: PF396P1D1
; CURRENT APPLICATION NUMBER: US/10/277,966
; CURRENT FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: 09/512,363
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/121,648
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/134,172
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: 60/144,076
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/176,200
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/063,212
; PRIOR FILING DATE: 1997-10-21
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 240
; TYPE: PRT
; ORGANISM: human
US-10-277-966-6

Query Match          92.0%; Score 1274.5; DB 14; Length 240;
Best Local Similarity 91.9%; Pred. No. 1.9e-97;
Matches 227; Conservative 1; Mismatches 0; Indels 19; Gaps 2;

QY 7 MGAFRALCGLLALCALSLGQRTGGPGCGPGRLLLTGTGDARCRVHTTRCCRDY----- 61
DB 1 MGAFRALCGLLALCALSLGQRTGGPGCGPGRLLLTGTGDARCRVHTTRCCRDYPAQLL 60
```

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 26, 2005, 15:38:30 ; Search time 25.693 Seconds
(without alignments)
902.513 Million cell updates/sec

Title: US-09-545-998B-4
Perfect score: 1386
Sequence: 1 MAQHGMGAFRALCGLALIC.....EEEGERSAEEKRLGLDW 241

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	197	14.2	256	2 B32393	T-cell antigen 4-1
2	195.5	14.1	255	2 I38426	lymphocyte activat
3	175	12.6	272	2 I48700	gene ox40 protein
4	168.5	12.2	271	2 S12783	OX40 antigen precu
5	162	11.7	277	2 I37552	OX40 homolog - hum
6	144.5	10.4	305	2 A46476	B cell-associated
7	139	10.0	295	2 JC5559	lectin-B - Virgini
8	134.5	9.7	1801	1 MWRTS	laminin beta-2 cha
9	133	9.6	435	2 I54182	tumor necrosis fac
10	130.5	9.4	651	2 JC7705	death receptor-6 -
11	129	9.3	461	1 A35366	tumor necrosis fac
12	127.5	9.2	1574	2 T13954	B-cell activation
13	124	8.9	277	2 A60771	gene murine tumor
14	121.5	8.8	459	2 I48854	tumor necrosis fac
15	121	8.7	474	2 B38634	laminin beta-2 cha
16	119.5	8.6	1798	2 S53869	laminin alpha 5 ch
17	119	8.6	3635	2 T10053	laminin beta-2 cha
18	118.5	8.5	1797	2 A55677	EGF repeat transme
19	117.5	8.5	1687	2 T30176	insulin-like growt
20	115.5	8.3	1371	2 A33837	insulin-like growt
21	114.5	8.3	329	2 A48805	hypothetical prote
22	112	8.1	152	2 T18975	hypothetical prote
23	111	8.0	1111	2 T26972	notch 3 protein -
24	111	8.0	2318	2 S45306	fibrillin-2 precu
25	110.5	8.0	2907	2 A57278	protein T22F7.3 [i
26	110	7.9	1522	2 H88380	hypothetical prote
27	109.5	7.9	164	2 T24272	notch-1 protein -
28	109.5	7.9	2531	2 A46019	apolipoprotein E r
29	109	7.9	996	2 J50237	

30 108 7.8 540 2 B47417 insulin receptor-x
31 106.5 7.7 2918 2 A54105 fibrillin-2 precu
32 106 7.6 788 2 T25061 hypothetical prote
33 105.5 7.6 1113 2 JE0315 low-density lipopr
34 105.5 7.6 1251 2 A57293 latent transformin
35 105 7.6 188 2 T15651 hypothetical prote
36 105 7.6 1172 1 TSHUP2 thrombospondin 2 p
37 105 7.6 3566 1 A40701 tenascin-X precurs
38 104.5 7.5 2825 2 T14271 Doc4 protein, stre
39 103.5 7.5 1737 2 T00209 MEGF8 protein - hu
40 102.5 7.4 770 2 T00204 LDL receptor-relat
41 102.5 7.4 770 2 T00203 LDL receptor-relat
42 102.5 7.4 956 1 A46016 thrombospondin 3
43 102 7.4 186 2 A28401 agglutinin isolect
44 102 7.4 1364 2 T00250 MEGF2 protein - hu
45 102 7.4 2871 2 A55567 fibrillin I - bovi

ALIGNMENTS

RESULT 1

B32393
T-cell antigen 4-1BB precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
C;Accession: B32393; I48879
R;Kwon, B.S.; Weissman, S.M.
Proc. Natl. Acad. Sci. U.S.A. 86, 1963-1967, 1989
A;Title: cDNA sequence of two inducible T-cell genes.
A;Reference number: A32393; MUID:89184547; PMID:2784565
A;Accession: B32393
A;Molecule type: mRNA
A;Residues: 1-256 <KWO>
A;Cross-references: UNIPROT:P20334; GB:J04492; NID:G201121; PIDN:AAA0167.1; PID:G201122
R;Kwon, B.S.; Kozak, C.A.; Kim, K.K.; Pickard, R.T.
J. Immunol. 152, 2256-2262, 1994
A;Title: Genomic Organization and Chromosomal Localization of the T-Cell Antigen 4-1BB.
A;Reference number: I48879; MUID:94179805; PMID:8133039
A;Accession: I48879
A;Status: preliminary; translated from GB/EMBL/DBD
A;Molecule type: DNA
A;Residues: 1-256 <RES>
A;Cross-references: EMBL:U02567; NID:g1117783; PIDN:AAA93113.1; PID:g409178
C;Genetics:
A;Introns: 35/1; 69/1; 115/1; 138/2; 156/3; 181/1; 225/1
C;Superfamily: CD27 antigen; NGF receptor repeat homology
C;Keywords: transmembrane protein
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-256/Product: 4-1BB protein #status predicted <MAT>

Query Match 14.2%; Score 197; DB 2; Length 256;
Best Local Similarity 28.8%; Pred. No. 2.9e-08;
Matches 64; Conservative 25; Mismatches 85; Indels 48; Gaps 10;

Qy 34 CGPGRLL-LTGTDGTCRCRVHTTCRCRDYPCGECSEW---DCMCVQPEFHCGDPCCITTC 89
Db 47 CPSTFSSIGQPCNCIRV-----CAGYFRFKFCSTHNAECIE-GFHCLGPQCITRC 101
Qy 90 RHHPCCPGQGVQSGKFSFGQICDASGTFSSGH-EGHCKPWTCTQFGELTVPPGNKT 148
Db 102 -EKDCRFGQLTKG-----CKTCSLGTFTNDQNGTGVCRPTNCSLDGRSLVKGTGTE 153
Qy 149 HNAVVCVP-----GSPPAEPGLGWTVVLLVAACVLLTSLQGLHITWQL 192
Db 154 KDVVCGPVPVWSFSPSTTISVTPGPGGSHSLQVLTFLALTSLALLAL-----IFITLL 207
Qy 193 RSQCMWPRETQLLEVP-----STEDARSCQFPPEERG 226
Db 208 FSVLKWRKKFPFHIFKFFKTTTGAAQEEACSCRCFOEEG 249

RESULT 2

I38426
Lymphocyte activation-induced receptor ILA precursor - human
C:Species: Homo sapiens (man)
C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C:Accession: I38426; J07052
R:Alderson, M.R.; Smith, C.A.; Tough, T.W.; Davis-Smith, T.; Armitage, R.J.; Falk, B.; R
Eur. J. Immunol. 24, 2219-2227, 1994
A:Title: Molecular and biological characterization of human 4-1BB and its ligand.
A:Reference number: I38426; MUID:94374434; PMID:8088337
A:Accession: I38426
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-255 <RES>
A:Cross-references: UNIPROT:Q07011; EMBL:U03397; NID:G571320; PIDN:AAAS3133.1; PID:G5713
R:Schwarz, H.; Tuckwell, J.; Lotz, M.
Gene 134, 295-298, 1993
A:Title: A receptor induced by lymphocyte activation (ILA): a new member of the human ne
A:Reference number: J07052; MUID:94085794; PMID:8262389
A:Accession: J07052
A:Molecule type: mRNA
A:Residues: 1-106, 'R', 108-255 <SCH>
C:Comment: This protein belongs to a member of the human nerve-growth-factor/tumor-necro
C:Comment: This receptor recognizes soluble, cell-surface bound or extracellular matrix
C:Superfamily: CD27 antigen; NGF receptor repeat homology
C:Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-255/Product: lymphocyte activation-induced receptor ILA #status predicted <MAT>
F:187-213/Domain: transmembrane #status predicted <TMM>
F:138,149/Binding site: carboxylate (Asn) (covalent) #status predicted
F:234,235/Binding site: phosphate (Thr) (covalent) (by casein kinase II) #status predict
F:242/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

Query Match 14.1%; Score 195.5; DB 2; Length 255;
Best Local Similarity 28.8%; Pred. No. 3.8e-08;
Matches 66; Conservative 21; Mismatches 81; Indels 61; Gaps 12;
QY 34 CGPGRLLLTGTGDARCCRVHTRCCRDYDG-----EECCS-----EWDNCVQPEFHCGDP 84
DB 48 CPNPSFSSAGG--QRTCDI-----CQCKGVFTRKECSSTNAECDC---TPGFHCLGA 97
QY 85 CCTTCRHHPCPGQVQSQGKFSFGQCLDCASGTFSGGHEGCKPWTCTQFGFLTVP 144
DB 98 GCSMC-EQCKQGOELTKG-----CKDCFGTFNDQKRGICRPWNCSDLGKSVLVN 149
QY 145 GNKTHNAVCPG-----SPPA---EPGLWLTVV--LLAVAACVLLTSAQLGLH 188
DB 150 GTERDVCVCGSPADLSPGASSVTPPAPAREPGHSPQIIISFFLALTSTALLFLFLTLR 209
QY 189 -----IWQLRSQCMWPRETOLLLEVPSTEDARSCQPPBEERG 226
DB 210 FSVVKGRRKKLLYIFKQFMRPVQT-----TQEDGCGSCRRPBEERG 251

RESULT 3
I48700
Gene ox40 protein - mouse
N:Alternate names: Ox40 antigen
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I48700; I48334; S34377
R:Calderhead, D.M.; Buhlmann, J.E.; van den Eertwegh, A.J.; Claassen, E.; Noelle, R.J.;
J. Immunol. 151, 5261-5271, 1993
A:Title: Cloning of mouse Ox40: a T cell activation marker that may mediate T-B cell int
A:Reference number: I48700; MUID:94044750; PMID:8228223
A:Accession: I48700
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-272 <RES>
A:Cross-references: UNIPROT:P47741; EMBL:Z21674; NID:G312827; PIDN:CAA79772.1; PID:G3128
R:Birkeland, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N.
Eur. J. Immunol. 25, 926-930, 1995
A:Title: Gene structure and chromosomal localization of the mouse homologue of rat Ox40
A:Reference number: I48334; MUID:95255413; PMID:7737295

A:Accession: I48334
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-14, 'G', 16-272 <RE2>
A:Cross-references: EMBL:X85214; NID:G732818; PIDN:CAA59476.1; PID:G732819
C:Genetics:
A:Gene: Ox40
A:Introns: 45/1; 86/1; 122/1; 144/2; 210/1; 250/1
C:Superfamily: CD27 antigen; NGF receptor repeat homology

Query Match 12.6%; Score 175; DB 2; Length 272;
Best Local Similarity 26.7%; Pred. No. 1.6e-06;
Matches 58; Conservative 19; Mismatches 70; Indels 70; Gaps 10;
QY 39 LLLGTGTAR--CCRVHT-----TRCRD-YPG-----EECCSEWDCMCVQPEFHCGDPC-- 85
DB 14 LALTLGVTAARLNCVKHTYPSGHKKCCRCQPGHGMVSRCDHTRDTLC-----HPCST 65
QY 86 -----CTTCRHHP-----CPPGQGVQSQGKFSFGQCID 114
DB 66 GFYNNAVNDYCKQCTQCNRHSGSELKNCNCTPTQDTVCRCRPGTQPRQDSGYKLGVDVCP 125
QY 115 CASGTFSGGHEGCHCKPWTCTQFGFLTVPFGNKNTHNAVCPGSPPAEPLGLWLTVVLLAVA 174
DB 126 CPPGHFSPGNNAQCKPWNCTLSGKQTRHPASDSLDAVCEDRS-----LLA-- 171
QY 175 ACVLLTSAQLGLHIVQWRSQCMWPRETOLLLEVPSP 211
DB 172 --LLIWEQRTFRPTTQSTTVMPTSE--LPSPT 204

RESULT 4
S12783
OX40 antigen precursor - rat
N:Alternate names: nerve growth factor receptor homolog
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: S12783; S08036
R:Mallett, S.; Fossum, S.; Barclay, A.N.
EMBO J. 9, 1063-1068, 1990
A:Title: Characterization of the MRC OX40 antigen of activated CD4 positive T lymphocytes
A:Reference number: S12783; MUID:90214614; PMID:2157591
A:Accession: S12783
A:Molecule type: mRNA
A:Residues: 1-271 <NAL>
A:Cross-references: UNIPROT:P15725; EMBL:X17037; NID:G57830; PIDN:CAA34897.1; PID:G57831
C:Superfamily: CD27 antigen; NGF receptor repeat homology
C:Keywords: growth factor receptor; transmembrane protein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-271/Product: OX40 antigen #status predicted <MAT>
F:211-235/Domain: transmembrane #status predicted <TMM>

Query Match 12.2%; Score 168.5; DB 2; Length 271;
Best Local Similarity 27.7%; Pred. No. 4.9e-06;
Matches 62; Conservative 17; Mismatches 80; Indels 65; Gaps 11;
QY 26 QRTPGCGGCGPGRLLLG--TGTDARCCRVHT-----RCCRD-YPGEECCSEWD----- 71
DB 6 QQPT-----AFLLLGLSLGVTVKLVNCKVOTYPSGHKKCCRCQPGHGMVSRCDHTRDTV 58
QY 72 CMCVQPEFHCG---DPC--CTTCRH-----PCPPGQGVQSQGKFSF 108
DB 59 CHPCPEPGFNEAVNYDTCKQCQCNHRSGSELKQNCPTPTEDVTCRCRPGTQPRQDSHKL 118
QY 109 GFQCIDCASGTFSGGHEGCKPWTCTQFGFLTVPFGNKNTHNAVCPGSPPAEPLGLWLTV 168
DB 119 GVDVCPGPGHSPGNSQACKPWNCTLSGKQIRHPASNSLDTVCEDRS----- 167
QY 169 VLLAVAAVCVLLTSAQLGLHIVQWRSQCMWPRETOLLLEVPSP 212
DB 168 --LLA---TLLIWEQRTFRPTTQSTTVMPTSE--LPSPT 201

```

RESULT 5
Ox40 homolog - human
C:Species: Homo sapiens (man)
C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C:Accession: I37552
R:Latza, U.; Durkop, H.; Schnitzger, S.; Ringeling, J.; Eitelbach, F.; Hummel, M.; Fonat
Eur. J. Immunol. 24, 677-683, 1994
A:Title: The human Ox40 homolog: cDNA structure, expression and chromosomal assignment
A:Reference number: I37552; MUID:94170844; PMID:7510240
A:Accession: I37552
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-277 <RES>
A:Cross-references: UNIPROT:P43489; EMBL:X75962; NID:g472957; PIDN:CAA53576.1; PID:g4729
C:Superfamily: CD27 antigen; NGF receptor repeat homology

Query Match 11.7%; Score 162; DB 2; Length 277;
Best Local Similarity 29.7%; Pred. No. 1.6e-05;
Matches 51; Conservative 11; Mismatches 92; Indels 18; Gaps 5;

QY 5 GAGAFRALCGALLCALSLG-----QRTPGCGGCGRLLGLGTGTDARCRVIT 54
DB 4 GARRLGRGFCALLLLGLSTVGLRVCVDTYPSNDRCHCECR--PGNGMVSRCRSQ 61
QY 55 TRCCRDYPG--RECCSEWDM-CVQEPFHCGD---PCCTTCRHHPCCPGGQVSGQKFSF 108
DB 62 TVCRPCGPGFYNDVSSKCPKCTWCNLSRSGSERKOLCTATQTVCRAGTQPLDSYKP 121
QY 109 GFQICIDASGTSGGHGHCKPWTCTQFGFLTVPFGNKNTHNAVCPVSGPPA 160
DB 122 GVDCAFCPGHFSFGDNQACKPWTNCTLAGKHTLPASNSDAICDRDPPA 173

RESULT 6
A46476
B cell-associated surface molecule CD40, long splice form - mouse
C:Species: Mus musculus (house mouse)
C>Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A46476; A46515
R:Torres, R.M.; Clark, E.A.
J. Immunol. 148, 620-626, 1992
A:Title: Differential increase of an alternatively polyadenylated mRNA species of murine
A:Reference number: A46476; MUID:92105763; PMID:1370315
A:Accession: A46476
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-305 <TOR>
A:Cross-references: UNIPROT:P27512; GB:M83312; NID:gl1553058
A>Note: sequence extracted from NCBI backbone (NCBIN:75206, NCBI:P:75207)
R:Grimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Cockayne,
J. Immunol. 149, 3921-3926, 1992
A:Title: Genomic structure and chromosomal mapping of the murine CD40 gene.
A:Reference number: A46515; MUID:93094586; PMID:1261194
A:Accession: A46515
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-287, 'LV' <GRI>
A:Cross-references: GB:M83312; NID:gl1553058; PIDN:AAB08705.1; PID:gl1553059; GB:M94126; N
A:Experimental source: BALB/c, liver
A>Note: sequence extracted from NCBI backbone (NCBI:P:120357)
C:Comment: For an alternative splice form, see PIR:A46515.
C:Comment: For an alternative splice form, see PIR:A46476.
C:Superfamily: CD27 antigen; NGF receptor repeat homology
C:Keywords: alternative splicing; transmembrane protein
F:105-144/Domain: NGF receptor repeat homology <NGF>

Query Match 10.4%; Score 144.5; DB 2; Length 305;
Best Local Similarity 22.8%; Pred. No. 0.00039;
Matches 65; Conservative 27; Mismatches 104; Indels 89; Gaps 12;

QY 13 LCGLL--ALLCALSLGQRPTGPGCGRLLGLGTGTDARCC----- 50

```

```

DB 7 LCAWGCCLLTAVHLGQCVT---CSDKOYL-----HDGQCCLDQPSRLTSHCTALEKTO 58
QY 51 -----RVHTTRCCRDYPG---EECCSEWDMCVQPE--FHCGBPCCCTT 88
DB 59 CHPCDSGFSQWNRREICHOHRHCEPNQGLRVKKEGTAESDTVCTCKGQHCTSKDCEA 118
QY 89 C-RHHPCCPGGQVSGQKFSFGQFCIDCASGTFSGHE--GHCKPWTCTQFGFLTVPFG 145
DB 119 CAQHTPCIPGFGVMEMATETTDTVCHPCVPVGFSNQSSILFEKCYPTWTSCEKKNLEVLQKG 178
QY 146 KNTHNAVCPGSPAPPEPLGWLTVLLAAVACVLLTSAQLGLHIWQLRSQCMWPRETOLL 205
DB 179 TSQTNVICGLKSR-----MRALLVIVVMGILITIFGVFLYIKRVVKK---PKDNEML 228
QY 206 LEVRPST-----EDARSCQFPPEERBERS 229
DB 229 ---PPAARRQDQEMEDYFGHTAAPVQETLHGCGQPVTCEDGKES 270

RESULT 7
JC5559
lectin-B - Virginian pokeweed
C:Species: Phytolacca americana (Virginian pokeweed)
C>Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 09-Jul-2004
C:Accession: JC5559
R:Yamaguchi, K.; Yurino, N.; Kino, M.; Ishiguro, M.; Funatsu, G.
Biosci. Biotechnol. Biochem. 61, 690-698, 1997
A:Title: The amino acid sequence of mitogenic lectin-B from the roots of pokeweed (Phyto)
A:Reference number: JC5559; MUID:97290889; PMID:9145528
A:Accession: JC5559
A:Molecule type: protein
A:Residues: 1-295 <YAM>
A:Cross-references: UNIPROT:Q9AVB0
A:Experimental source: root
C:Comment: This protein is a lectin specific for N-acetylglucosamine-containing saccharide
C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl
C:Keywords: glycoprotein
F:96,139/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.0%; Score 139; DB 2; Length 295;
Best Local Similarity 28.8%; Pred. No. 0.001;
Matches 36; Conservative 18; Mismatches 41; Indels 30; Gaps 8;

QY 20 CALSLGQRPTGPG-----GCGPGRLLGLGTGTDARCCRVHTTRCCRDYPG-----EECC 67
DB 133 CGVDFGNRTCPNDLCCSEWGCIGITGCGEQSQSC---NHQRCGKDFAGRTCLNDLCC 189
QY 68 SEWDMCVQPEFHCGBPCCCTTCRHHPCCPGGQVSGQKFSFGQ-C---IDCASGTFSGG 123
DB 190 SEWG-WCGSSEAHCQCGQSCQNCNRYNC-----GR-NFGPRTCPNELCCSSGGWCGS 238
QY 124 HEGHC 128
DB 239 NDAHC 243

RESULT 8
MMRTS.
laminin beta-2 chain precursor - rat
N:Alternate names: laminin chain B3; S-laminin
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
C:Accession: S03539
R:Hunter, D.D.; Shah, V.; Merlie, J.P.; Sanes, J.R.
Nature 338, 229-234, 1989
A:Title: A laminin-like adhesive protein concentrated in the synaptic cleft of the neuron
A:Reference number: S03539; MUID:89159410; PMID:2922051
A:Accession: S03539
A:Molecule type: mRNA
A:Residues: 1-1801 <HUN>
A:Cross-references: UNIPROT:P15800; EMBL:X16563; NID:957250; PIDN:CAA34561.1; PID:957251
C:Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin (

```

C:Function:

A:Description: interact with cells and with other basement membrane proteins to promote C:Superfamily: laminin beta-1 chain; laminin-type EGF-like homology C:Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular F:1-35/Domain: signal sequence #status predicted <SIG> F:36-1801/Product: laminin beta-2 chain #status predicted <MAT> F:36-285/Domain: VI <DOM6> F:286-555/Domain: V <DOM5> F:286-347/Domain: laminin-type EGF-like homology <LE01> F:350-410/Domain: laminin-type EGF-like homology <LE02> F:413-470/Domain: laminin-type EGF-like homology <LE03> F:473-522/Domain: laminin-type EGF-like homology <LE04> F:525-555/Domain: laminin-type EGF-like homology #status atypical <LE05> F:556-784/Domain: IV <DOM4> F:786-831/Domain: laminin-type EGF-like homology <LE06> F:788-1196/Domain: III <DOM3> F:834-877/Domain: laminin-type EGF-like homology <LE07> F:880-927/Domain: laminin-type EGF-like homology <LE08> F:930-986/Domain: laminin-type EGF-like homology <LE09> F:989-1038/Domain: laminin-type EGF-like homology <LE10> F:1041-1095/Domain: laminin-type EGF-like homology <LE11> F:1098-1143/Domain: laminin-type EGF-like homology <LE12> F:1146-1190/Domain: laminin-type EGF-like homology <LE13> F:1197-1412/Domain: II <DOM2> F:1197-1412/Region: heptad repeats F:1413-1445/Domain: alpha <ALP> F:1446-1801/Region: heptad repeats F:1446-1801/Domain: I <DOM1> F:45-50/disulfide bonds: #status predicted F:45-371,1088,1252,1311,1351,1502/binding site: carbohydrate (Asn) (covalent) #status F:1193,1196,1800/disulfide bonds: interchain #status predicted

Query Match 9.7%; Score 134.5; DB 1; Length 1801;
Best Local Similarity 26.9%; Pred. No. 0.0088;
Matches 63; Conservative 6; Mismatches 60; Indels 105; Gaps 15;
QY 8 GAFRALC-GLALLCALSLG-----QRPTGG-PGCGP-----GRLLLGTTGTARCCRV 52
DB 840 GALSALCEGTSQCLRTGAFGLRCDHCQRGWGPFNCPCVGNR-----ADECDA 891
QY 53 HTTRC---CHDYGERCCSWDCMCVQPEPHCGDPCT---TCRHHPCPGQGVQSGKFS 107
DB 892 HTGACLGCRDYGGEHCER-----CI-AGFH-GDPRLPYGGQCRPCPCPEPG--SQRHFA 943
QY 108 -----FGQCICDCASGTF----- 120
DB 944 TSCHRDGYQQIVCHRCAGYTLGRCEACAPGHFGDPSKPGRCQLCECSGNIDPTDPGAC 1003
QY 121 -----SGGHEGHCXKPTWDTCTQFGFLTVPFGNKTNNAVC-VPGSP 159
DB 1004 DPHTGQCLRLHHTGPHGCHKP-----GFHGQAARQSCHRCTCNLLGTD 1050

RESULT 9
154182
tumor necrosis factor receptor 2-related protein - human
C:Species: Homo sapiens (man)
C:Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
C:Accession: I54182
R:Baens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.
Genomics 16, 214-218, 1993
A:Title: Construction and evaluation of a hncDNA library of human 12p transcribed sequen
A:Reference number: I54182; MUID:93252381; PMID:8486360
A:Accession: I54182
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-435 <RES>
A/Cross-references: UNIPROT:P36941; GB:L04270; NID:g339761; PIDN:AAA36757.1; PID:g339762
C:Genetics:
A:Gene: GDB:UTBR
A/Cross-references: GDB:1230195; OMIM:600979
A:Map position: 12p13.3-12p13.1
C:Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolo

Query Match 9.6%; Score 133; DB 2; Length 435;
Best Local Similarity 25.0%; Pred. No. 0.004;
Matches 57; Conservative 17; Mismatches 86; Indels 68; Gaps 13;
QY 34 CGPGRLLLTGTDARCCRVHTTRC-----CRDYPGEE---C 66
DB 62 CPP-----GTVVSACKSRIDTVCATCAENSYNEHWNVLTICQLCRPCDPVWGLBEIAPC 116
QY 67 CS--EWDCMCVQPEFHCGDPC--CTTCR-HHPCPPGQGVQSGKFSFG-FQCIDCASGTF 120
DB 117 TSKRKTQCR-QPGWFCAAWALECTHCELLSDCPGTEALNKDEVGKGNHCVCKAGHF 175
QY 121 --SGGHEGHCXKPTWDTCTQFGFLTVPFGNKTNNAVCVGSPPAEPGLG-----WLTVVLL 171
DB 176 QNTSSPSARCQPHTRCENQGLVEAAGTAQSDTTT---KNPLEPLPPEMMSGTMLLAVLL 232
QY 172 AVAACVLLLTSAQLGLHQLRSOCMPRETQL-----LLEVPSPSTE 213
DB 233 PLAFLLLATV-----FSCIWKSHPSLCKRLGSLKKRRPQGE 269
RESULT 10
JC7705
death receptor-6 - chicken
C:Species: Gallus gallus (chicken)
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Jul-2004
C:Accession: JC7705
R:Bridgman, J.T.; Bohe, J.; Goetz, F.W.; Johnson, A.L.
Biochem. Biophys. Res. Commun. 284, 1109-1115, 2001
A:Title: Conservation of death receptor-6 in avian and piscine vertebrates.
A:Reference number: JC7705; MUID:21308433; PMID:11414698
A:Accession: JC7705
A:Molecule type: mRNA
A:Residues: 1-651 <BRI>
A/Cross-references: UNIPROT:Q98SM6; GB:AF349908
C:Comment: this receptor, a member of the tumor necrosis factor receptor family, belongs
tresa, activates a cell death and/or survival signaling cascade.
C:Genetics:
A:Gene: dr-6
C:Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolo
C:Keywords: ovary
F:1-21/Domain: signal sequence #status predicted <SIG>
F:52-196/Domain: extracellular cysteine-rich, ligand-binding #status predicted <ECU>
F:332-350/Domain: transmembrane #status predicted <TM>
F:410-475/Domain: death domain #status predicted <DED>
F:551-651/Region: conserved cytoplasmic #status predicted

Query Match 9.4%; Score 130.5; DB 2; Length 651;
Best Local Similarity 29.8%; Pred. No. 0.0084;
Matches 39; Conservative 14; Mismatches 55; Indels 23; Gaps 6;
QY 48 RC-CR-----VHTTRCCRDYPGEECCSWDCMCVQPEPHCGDPCTTCRHHPCPGQ 98
DB 90 RCHPCRKPCCLPMIEKTHC-----TALTDRECTCLSGTFQINDTCVP---YTVCPVW 139
QY 99 GVQSGKFSFGQCICDCASGTFSGGHEG--HCKPMTDCTQFGFLTVPFGNKTNNAVCVPG 156
DB 140 GVRKGTETEDVRCKPCPLRGTFSDVPSSVMKCTVTDTCFGKNMVVVKPGTKESDNVC--X 197
QY 157 SPPAEPGLGWL 167
DB 198 SPASLPNTSLT 208

RESULT 11
A35356
tumor necrosis factor receptor 2 precursor [validated] - human
N/Alternate names: 75K tumor necrosis factor receptor; TNF receptor type 2
C:Species: Homo sapiens (man)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A35356; A36475; A48416; A36007; A23666; B35010; I38094
R:Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower, S.K.

Science 248, 1019-1023, 1990
A:Title: A receptor for tumor necrosis factor defines an unusual family of cellular and
A:Reference number: A33556; MUID:90260639; PMID:2160731
A:Accession: A33556
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-461 <SMI>
A:Cross-references: UNIPROT:P20333; GB:M32315; NID:g189185; PIDN:AAA59929.1; PID:g189186
R:Kohn, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squires,
Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990
A:Title: A second tumor necrosis factor receptor gene product can shed a naturally occur
A:Reference number: A36475; MUID:91045991; PMID:2172983
A:Accession: A36475
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-195, 'R', 197-461 <KOH>
A:Cross-references: GB:M55994; GB:M38549; NID:g339757; PIDN:AAA36755.1; PID:g339758
R:Dembic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus, M.
Cytokine 2, 231-237, 1990
A:Title: Two human TNF receptors have similar extracellular, but distinct intracellular,
A:Reference number: A48416; MUID:91370690; PMID:1966549
A:Accession: A48416
A>Status: preliminary
A:Molecule type: protein
A:Residues: 23-461 <DEM>
A:Cross-references: GB:S63368; NID:g235648; PIDN:AAB19824.1; PID:g235649
A>Note: sequence extracted from NCBI backbone (NCBIN:63368, NCBI:P:63371)
R:Heiler, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M.
Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990
A:Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demonstra
A:Reference number: A36007; MUID:90349572; PMID:2166646
A:Accession: A36007
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 116-140, 'P', 142-195, 'R', 197-362, 'T', 364-461 <HEL>
A:Cross-references: GB:M35857; NID:g339751; PIDN:AAA63262.1; PID:g339752
R:Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M.
J. Biol. Chem. 265, 20131-20138, 1990
A:Title: Purification and partial amino acid sequence analysis of two distinct tumor nec
A:Reference number: A23666; MUID:91056048; PMID:2173696
A:Accession: A23666
A>Status: preliminary
A:Molecule type: protein
A:Residues: 23-40; 65-69; 136-141; 300-306 <LOB>
R:Engelmann, H.; Novick, D.; Wallach, D.
J. Biol. Chem. 265, 1531-1536, 1990
A:Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence
A:Reference number: A35010; MUID:90110215; PMID:2153136
A:Accession: B35010
A>Status: preliminary
A:Molecule type: protein
A:Residues: 27-31 <ENG>
R:Kuhnert, P.; Kemper, O.; Wallach, D.
Gene 150, 381-386, 1994
A:Title: Cloning, sequencing and partial functional characterization of the 5' region of
A:Accession: I38094
A:Reference number: I38094; MUID:95121934; PMID:7821811
A:Molecule type: DNA
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Residues: 1-37 <RES>
A:Cross-references: EMBL:X80021; NID:g666044; PIDN:CAA56324.1; PID:g825701
C:Genetics:
A:Gene: GDB:TNFR2
A:Cross-references: GDB:125914; OMIM:191191
A:Map position: 1p36.2-1p36.2
A:Introns: 26/3
A>Note: the list of introns is incomplete
C:Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homolo
C:Keywords: duplication; glycoprotein; receptor; transmembrane protein
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-416/Product: tumor necrosis factor receptor 2 #status experimental <MAT>
F:40-76/Domain: NGF receptor repeat homology <NG1>
F:78-119/Domain: NGF receptor repeat homology <NG2>

F:120-162/Domain: NGF receptor repeat homology <NG3>
F:164-201/Domain: NGF receptor repeat homology <NG4>
F:262-279/Domain: transmembrane #status predicted <TMN>
F:280-461/Domain: intracellular #status predicted <INT>
F:171,193/Binding site: carbohydrate (Asn) (covalent) #status predicted

QY	34	CGPG--	RLLLGTGTDARC	9.3%;	Score 129;	DB 1;	Length 461;
Db	57	CSPGQAKVCTKTSDTVCDSCEDSTYTQWVPECLSCGRCSDDQVETQACTFEQNR	116				
QY	72	-CMCVQPEFHC	-----GDPCTTCRHHPCPPGQVQSQGKFSFGQCICDASGTFSG--	122			
Db	117	ITC-TPGMYCALSKOEGCLCAPLR--KCRPGFVGARFGTETSDVCKPCAPGTFSNTT	173				
QY	123	GHEGCKPWTCTQFGFLTVFPGNTHNAV	-----VPG-----	156			
Db	174	SSTDICRPHQICN-----VVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQP	229				
QY	157	-----SPRAE-----PLGW-----LTVLLAAVAAVLLLTSAQ	184				
Db	230	TPEPSTAPSTFLLPMGPSPPAEGSGDPALPVGLIVGTALGLLIIGVNVCMINT----	285				
QY	185	LGLHIWQLRSQCMWPRETQLLLEVPSTED-ARSCQFPREE	224				
Db	286	-----QVKKK-----PLCLQREAKVPHLPADKARGTQGPQQ	317				

RESULT 12
T13954
MEGF6 protein - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T13954
R:Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
Genomics 51, 27-34, 1998
A:Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
A:Reference number: Z14126; MUID:98360089; PMID:9693030
A:Accession: T13954
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1574 <NAK>
A:Cross-references: UNIPROT:O88281; EMBL:AB011532; NID:g3449293; PIDN:BAA32462.1; PID:g34
A:Experimental source: strain Sprague-Dawley; brain
C:Genetics:
A:Gene: MEGF6

QY <th>45 <th>TDARCCRVHTTRCCRDY</th> <th>---PGEE--CCSEWDCMCVQPEFHC</th> <th>9.2%;</th> <th>Score 127.5;</th> <th>DB 2;</th> <th>Length 1574;</th> </th>	45 <th>TDARCCRVHTTRCCRDY</th> <th>---PGEE--CCSEWDCMCVQPEFHC</th> <th>9.2%;</th> <th>Score 127.5;</th> <th>DB 2;</th> <th>Length 1574;</th>	TDARCCRVHTTRCCRDY	---PGEE--CCSEWDCMCVQPEFHC	9.2%;	Score 127.5;	DB 2;	Length 1574;
Db	99	TEART-----VFRCCPGWSQKPGQEGCLSDVD--ECASANGGCEGPGCCNTVGGFYCR--	CP 150				
QY	96	PGQGVQSQGKFSFGQICDASGTFSGGHGHCKPWTCTQFGFLTVFPGNTHNAV	CVP 155				
Db	151	PGYQLQGDGK-----TCQDVDECAHNGGQ-----	HRCVNT 183				
QY	156	GS-----PRAEPLGWLTVLLAAVAAVLLLTSAQ-----LGLHIWQLRSQCMWPRETQLLLE	207				
Db	184	GSYLCECKPFGRLHTDGRCTCLAISSCTLNGGCGQHCQVQLTVTHRCQCRPQLQ-----	239				
QY	208	VPESTEDARSC	218				
Db	240	-----EDGRC	245				

RESULT 13
A60771

156	APNGVLKACAPCTGSDTTSTSDVCRPHRCS---	ILAI	PGNASTDAV	CAPESPTLSA	211
159	-----PAE-----	-----	-----	PLGW-----	165
212	IPRTLVSQPEPTRSQPLDQPGSPQSILTS	LGSTPI	IEQSTKG	GISLPIGLIVG	271
166	LTVVLLAVACVLLLTSAQLGL-----	HIQL	RSQCWP	PRETOLLLEVP	213
272	LGILMLGVNCIILVQRKKPSCILQRDAK	VPVDEK	SQDAVGLE	QQHLLTTP	331
214	-----DARS-----	COFPE	ERCER	SAEEKRLGD	238
332	LESSASAGDRRAPPGHGPQARVMAE	AQGFQ	BARASSRISD	371	

Search completed: October 26, 2005, 15:52:34
Job time : 26.693 secs

THIS PAGE BLANK (USP 10)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 26, 2005, 15:29:08 ; Search time 118.701 Seconds
(without alignments)
1039.676 Million cell updates/sec

Title: US-09-545-998B-4
Perfect score: 1386
Sequence: 1 MAQHGAMGAFRALCGLALIC.....EEBGRSAAEKRLGLDW 241

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 03:.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1386	100.0	241	1 TR18 HUMAN	Q9Y5U5 homo sapien
2	735.5	53.1	228	1 TR18_MOUSE	Q35714 mus musculus
3	735.5	53.1	250	2 Q8C4K3	Q8C4K3 mus musculus
4	202	14.6	275	2 Q80WM9	Q80WM9 mus musculus
5	201.5	14.5	276	2 Q71F55	Q71F55 mus musculus
6	197	14.2	256	1 TNR9_MOUSE	P20334 mus musculus
7	195.5	14.1	255	1 TNR9_HUMAN	Q07011 homo sapien
8	191	13.8	270	2 Q75SV8	Q75SV8 felis silve
9	182.5	13.2	290	2 Q76L84	Q76L84 paralichthy
10	182	13.1	267	2 Q02764	Q02764 oryctolagus
11	177	12.8	276	2 Q9DDD2	Q9DDD2 gallus gall
12	175	12.6	272	1 TNR4_MOUSE	P47741 mus musculus
13	174.5	12.6	196	2 Q8VC17	Q8VC17 mus musculus
14	170.5	12.3	211	2 Q8R037	Q8R037 mus musculus
15	170	12.3	274	2 Q7YR15	Q7YR15 canis famul
16	168.5	12.2	271	1 TNR4_RAT	P15725 rattus norv
17	162	11.7	277	1 TNR4_HUMAN	P43489 homo sapien
18	158.5	11.4	467	2 Q800T0	Q800T0 gallus gall
19	153	11.0	300	1 TF6B_HUMAN	Q95407 homo sapien
20	150	10.8	616	1 TR11_MOUSE	Q9Y6Q6 homo sapien
21	148.5	10.7	278	2 Q8SQ34	Q8SQ34 sus scrofa
22	146	10.5	401	2 Q6P112	Q6P112 mus musculus
23	144.5	10.4	289	1 TNR5_BOVIN	Q28203 bos taurus
24	144.5	10.4	269	1 TNR5_MOUSE	P27512 mus musculus
25	143.5	10.4	277	2 Q8WMQ2	Q8WMQ2 ovis aries
26	143.5	10.4	289	2 Q8K2X6	Q8K2X6 mus musculus
27	142	10.2	401	1 T11B_RAT	Q08727 rattus norv
28	142	10.2	483	2 Q800K7	Q800K7 paralichthy
29	141.5	10.2	169	2 Q9JKQ0	Q9JKQ0 rattus norv
30	141	10.2	401	1 T11B_MOUSE	Q08712 mus musculus
31	139.5	10.1	457	2 Q9IV56	Q9IV56 homo sapien

000300 homo sapien
Q98sm6 gallus gall
Q9avb0 phytolacca
Q7t2h3 oncorhynchu
Q6glh3 xenopus lae
Q35105 mus musculus
P15800 rattus norv
P36941 homo sapien
P50284 mus musculus
Q75509 homo sapien
P20333 h tumor nec
Q88281 rattus norv
Q61292 mus musculus
Q8r0y0 mus musculus

32 138 10.0 401 1 T11B HUMAN
33 137.5 9.9 651 2 Q98SM6
34 137 9.9 361 2 Q9AVB0
35 135.5 9.8 318 2 Q7T2H3
36 135.5 9.8 287 2 Q6GLH3
37 134.5 9.7 825 1 TR11_MOUSE
38 134.5 9.7 1801 1 TNR2_RAT
39 133 9.6 435 1 TNR3_HUMAN
40 130.5 9.4 415 1 TNR3_MOUSE
41 129.5 9.3 655 1 TR21_HUMAN
42 129 9.3 461 1 TR1B_HUMAN
43 127.5 9.2 1574 1 EFL3_RAT
44 127.5 9.2 1799 1 LMB2_MOUSE
45 126.5 9.1 1799 2 Q8R0Y0

ALIGNMENTS

RESULT 1
TR18 HUMAN STANDARD; PRT; 241 AA.
ID Q9Y5U5; Q98S61; Q9NY39;
AC Q9Y5U5; Q98S61; Q9NY39;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 18 precursor
DE (Glucocorticoid-induced TNFR-related protein) (Activation-inducible
DE TNFR family receptor) (UNQ319/PRO364).
DE Name=TNFRSF18; Synonyms=AITR, GTR;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND INTERACTIONS WITH TRAF1, TRAF2 AND TRAF3.
RC TISSUE=Bone marrow;
RX MEDLINE=99175482; PubMed=10074428; DOI=10.1016/S0960-9822(99)80093-1;
RA Gurney A.L., Marsters S.A., Huang R.M., Pitti R.M., Mark D.T.,
Baldwin D.T., Gray A.M., Dowd A.D., Brush A.D., Heldens A.D.,
Schow A.D., Goddard A.D., Wood W.I., Baker K.P., Godowski P.J.,
Ashkenazi A.;
RA "Identification of a new member of the tumor necrosis factor family
and its receptor, a human ortholog of mouse GITR.";
RL Curr. Biol. 9:215-218(1999).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=T-cell;
RX MEDLINE=99156876; PubMed=10037686; DOI=10.1074/jbc.274.10.6056;
RA Kwon B., Yu K.-Y., Ni J., Yu G.-L., Jang I.-K., Kim Y.-J., Xing L.,
Liu D., Wang S.-X., Kwon B.S.;
RA "Identification of a novel activation-inducible protein of the tumor
necrosis factor receptor superfamily and its ligand.";
RL J. Biol. Chem. 274:6056-6061(1999).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Thymus;
RX MEDLINE=20292073; PubMed=10936847;
RA Nacentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,
Brunetti L., Migliorati G., Riccardi C.;
RA "Identification of three novel mRNA splice variants of GITR.";
RL Cell Death Differ. 7:408-410(2000).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D.,

RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P., Gray A.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
RN [5]
RP SEQUENCE OF 26-40.
RX PubMed=15340161; DOI=10.1110/ps.04682504;
RA Zhang Z., Henzel W.J.;
RT "Signal peptide prediction based on analysis of experimentally
RT verified cleavage sites.";
RL Protein Sci. 13:2819-2824(2004).
CC -!- FUNCTION: Receptor for TNFRSF18. Seems to be involved in
CC interactions between activated T lymphocytes and endothelial cells
CC and in the regulation of T cell receptor-mediated cell death.
CC Mediated NF-kappa-B activation via the TRAF2/NIK pathway.
CC -!- SUBUNIT: Binds to TRAF1, TRAF2, and TRAF3, but not TRAF5 and
CC TRAF6.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1).
CC Secreted (isoform 2).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q9Y5U5-1; Sequence=Displayed;
CC Name=2; Synonyms=GITR-D;
CC IsoId=Q9Y5U5-2; Sequence=VSP_006508;
CC -!- TISSUE SPECIFICITY: Expressed in lymph node, peripheral blood
CC leukocytes and weakly in spleen.
CC -!- INDUCTION: Up-regulated in peripheral mononuclear cells after
CC antigen stimulation/lymphocyte activation.
CC -!- SIMILARITY: Contains 3 TNFR-Cys repeats.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>)
CC or send an email to license@isb-sib.ch.
CC -----
DR EMBL; AF125304; AAD2635.1; -;
DR EMBL; AF117297; AAD19694.1; -;
DR EMBL; AF241229; AAF63506.1; -;
DR EMBL; AY358877; AAO89236.1; -;
DR Genbank; HGNC:11914; TNFRSF18.
DR MIM; 603905; -;
DR GO; GO:0005031; P:tumor necrosis factor receptor activity; TAS.
DR GO; GO:0006916; P:anti-apoptosis; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPR001368; TNFR C6.
DR PROSITE; PS00652; TNFR_NGFR_1; FALSE_NEG.
DR PROSITE; PS50050; TNFR_NGFR_2; FALSE_NEG.
KW Alternative splicing; Direct protein sequencing; Glycoprotein;
KW Receptor; Repeat; Signal; Transmembrane.
FT SIGNAL 1 25
FT CHAIN 26 241 Tumor necrosis factor receptor
FT superfamily member 18.
FT DOMAIN 26 162 Extracellular (Potential).
FT TRANSNEM 163 183 Potential.
FT DOMAIN 184 241 Cytoplasmic (Potential).
FT REPEAT 34 72 TNFR-Cys 1.
FT REPEAT 74 112 TNFR-Cys 2.
FT REPEAT 115 153 TNFR-Cys 3.
FT DISULFID 34 49 By similarity.
FT DISULFID 74 86 By similarity.
FT DISULFID 81 94 By similarity.
FT DISULFID 115 134 By similarity.
FT DISULFID 128 153 By similarity.
FT CARBOHYD 146 146 N-linked (GlcNAc...) (Potential).
FT VARSPIC 135 241 TOPGFTVTPGKTNHNAVCPGSPPAEPLGMLTVVLLAVAA
SCFPPEERGERSAEKGRLGLDLMV -> CWRCKRRPKTPE

FT AASPRKSGSDRORRRGSGWETCGCEPRPGPPTAASPSP
FT GAPQAGALRSLGRALLPWQKQWQEGSGDORPGCSSAA
FT AAGPCRRERETQSNWPPSSLAGPDGVGS (in isoform
FT 2).
FT /FTid=VSP_006508.
FT SQ CONFLICT 194 201 SQMWPRE -> K (in Ref. 2).
FT SEQUENCE 241 AA; 26000 MW; 90DC3B4AA7E82CBE CRC64;
Query Match 100.0%; Score 1386; DB 1; Length 241;
Best Local Similarity 100.0%; Pred. No. 9.9e-110;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAQHGMCAFRALCGALLCALSLGQRTGGPGCGPGRLLLTGTGDARCCRVHTRCCRD 60
DB 1 MAQHGMCAFRALCGALLCALSLGQRTGGPGCGPGRLLLTGTGDARCCRVHTRCCRD 60
QY 61 YPGECCSEWDCMCVQPEFHGCDPCTTCRHHPCPPGQGVQSGQKFSFGFCIDCASGTF 120
DB 61 YPGECCSEWDCMCVQPEFHGCDPCTTCRHHPCPPGQGVQSGQKFSFGFCIDCASGTF 120
QY 121 SGGHEGHCCKPMTDCTQFGFLTVFPGNKTHNAVCPGSPPAEPLGMLTVVLLAVAAVLL 180
DB 121 SGGHEGHCCKPMTDCTQFGFLTVFPGNKTHNAVCPGSPPAEPLGMLTVVLLAVAAVLL 180
QY 181 TSAQGLHIWQLRSQCMWPRETQLLLEVPSTEDARSCQFPEERGERSAEKGRLGLDLM 240
DB 181 TSAQGLHIWQLRSQCMWPRETQLLLEVPSTEDARSCQFPEERGERSAEKGRLGLDLM 240
QY 241 V 241
DB 241 V 241
RESULT 2
TR18 MOUSE
ID TR18 MOUSE STANDARD; PRT; 228 AA.
DT 035714; Q9JUKR1; Q9JUKR2; Q9JUKR3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 18 precursor
DE (Glucocorticoid-induced TNFR-related protein).
DE Name=tnfrsf18; Synonyms=Gitr;
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A. (ISOFORM A).
RC STRAIN=C3H;
RX MEDLINE=97322352; PubMed=9177197; DOI=10.1073/pnas.94.12.6216;
RA Nocentini G., Giunchi L., Ronchetti S., Krausz L.T., Bartoli A.,
RA Moraca R., Migliorati G., Riccardi C.;
RT "A new member of the tumor necrosis factor/nerve growth factor
RT receptor family inhibits T cell receptor-induced apoptosis.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:6216-6221(1997).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM A).
RC STRAIN=BALE/c;
RX MEDLINE=20256302; PubMed=10798444; DOI=10.1089/104454900314474;
RA Nocentini G., Bartoli A., Ronchetti S., Giunchi L., Cupelli A.,
RA Delfino D., Migliorati G., Riccardi C.;
RT "Gene structure and chromosomal assignment of mouse Gitr, a member of
RT the tumor necrosis factor/nerve growth factor receptor family.";
RL DNA Cell Biol. 19:205-217(2000).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS B; C AND D).
RC TISSUE=Thymus;
RX MEDLINE=20292073; PubMed=10836847;
RA Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,
RA Brunetti L., Migliorati G., Riccardi C.;
RT "Identification of three novel mRNA splice variants of Gitr.";
RL Cell Death Differ. 7:408-410(2000).

InterPro; IPR006210; IEGF.
DR DR SMART; IPR001368; TNFR_c6.
DR DR SMART; SM00181; EGF; 1.
DR DR SMART; SM00208; TNFR; 2.
DR DR PROSITE; PS00652; TNFR_NGFR_1; FALSE NEG.
DR DR PROSITE; PS00050; TNFR_NGFR_2; FALSE NEG.
KW KW Alternative splicing; Glycoprotein; Receptor; Repeat; Signal;
Transmembrane.
FT FT SIGNAL 1 19 Potential.
FT FT CHAIN 20 228 Tumor necrosis factor receptor
FT FT DOMAIN 20 153 superfamily member 18.
FT FT TRANSMEM 154 174 Extracellular (Potential).
FT FT DOMAIN 175 228 Potential.
FT FT REPEAT 28 61 Cytoplasmic (Potential).
FT FT REPEAT 62 101 TNFR-Cys 1.
FT FT REPEAT 102 142 TNFR-Cys 2.
FT FT DISULFID 29 44 TNFR-Cys 3.
FT FT DISULFID 62 74 By similarity.
FT FT DISULFID 69 82 By similarity.
FT FT DISULFID 103 122 By similarity.
FT FT DISULFID 116 141 By similarity.
FT FT CARBOHYD 36 36 N-linked (GLNac. .) (Potential).
FT FT CARBOHYD 40 40 N-linked (GLNac. .) (Potential).
FT FT CARBOHYD 121 121 N-linked (GLNac. .) (Potential).
FT FT CARBOHYD 134 134 N-linked (GLNac. .) (Potential).
FT FT VARSPLIC 121 228 NCSPQGLTWPGNKTNHNAVCIEPELPTQYGHLTIVFLVM
ACCFITLVTLVQLGHIWQLRRQMCPRETQPPFAEVLSAED
FT FT ACSCFPPEERGGTTEKHLGRWP -> KDPAIRGGAVV
S (in isoform D).
FT FT /FTId=VSP_006509.
FT FT VARSPLIC 189 228 ETOPPAEVOISAEADACSFPPEERGGTTEKCHLGGRWP
-> VLIIQRSHRRCSCQLMLLAASSIIRNAGSRQKSVI
FT FT WGVGGHEAMSSVPARRYKTCPAIPLVIRAGAMLUCTLPWAW
FT FT BCSPPQQWRKKVYSSELRLGPMAFLI (in isoform
B).
FT FT /FTId=VSP_006510.
FT FT VARSPLIC 189 228 ETOPPAEVOISAEADACSFPPEERGGTTEKCHLGGRWP
-> GQLCPREGENVSQPHILPQFYRDPAIRGGAVS (in
isoform C).
FT FT /FTId=VSP_006511.
FT FT SEQUENCE 228 AA; 25334 MW; 50D8C275D9C56259 CRC64;
Query Match 53.1%; Score 735.5; DB 1; Length 228;
Best Local Similarity 57.0%; Pred. No. 1.6e-54;
Matches 134; Conservative 31; Mismatches 61; Indels 9; Gaps 3

QY	7	MGAFRALCGIALLCALSIGQ-RPTGGPGCGPGRLLLTGTGDARCCRVHTTRCCRDYPGEE	65
Dd	1	MGAWAMLYGSMLCVLDLGPVSVEEFGCGPKVGNSGNTRCCSLYA-----PQKE	53
QY	66	CCSEWDCMCVQPFHFHCDDPCCTTCRHHPCPGPGVQSOGKFSFGQCICDSAGTFSGGHE	125
Dd	54	DCPKERICVTPEYHCGDPCKICKHPYCQPQGRVESQSDIVDFGRFCVACAMGTFPSAGR	113
QY	126	GHKXPWTCDTQGFGLTVFPNGKNTHNAVCPGPSPPAEPLMGLMTVVLLAVAACVILLTSQAL	185
Dd	114	GHCLRWNCNQGFGLTWFPNGKNTHNAVCIPEPLPTQYGHLTIVFLVMAACIFLTTVOL	173
QY	186	GLHTWLRSOCMPRETQLLEVPSPTEDARSQCFPEERGERSAEKGRGLDW	240
Dd	174	GLHIWLRQHMCPRTPQPPAEVOLSADACSFPPEERGEQT-EKCHLGGRW	227

RESULT 3
Q8C4K3 PRELIMINARY; PRT; 250 AA.

ID	Q8C4K3	PRELIMINARY;	PRT;	250 AA.
AC	Q8C4K3;			
DT	01-MAR-2003	(TrEMBLrel. 23, Created)		
DT	01-MAR-2003	(TrEMBLrel. 23, Last sequence update)		
DT	01-MAR-2004	(TrEMBLrel. 26, Last annotation update)		
DE	Mus musculus	16 days embryo head cDNA, RIKEN full-length enriched		
DE	library, clone:C130084C11	product:tumor necrosis factor receptor		


```
QY 95 PPGQGVOSQKFSFGQICDASCTPS-CGHEGCHKPWTDCQTQPGFLTVFPGNKTNAV 153
Db 145 PPGQVRKRGTHDQDVTVCADCTGTGSLGGTQBECLPWTNCSAFQ-QEVRRTGNTSDTTC 203
QY 154 VPGSPAPBLGMLTVLLAV----AACVLLTSAQLGLHIWLQRSQCMWPRETQLLLV 209
Db 204 -----SSQVYVVVSVLLPLVIVGAGIAGFLICTRRLHTSSVAK 247
QY 210 PSTEDARSCOPPEERGERSAEBK 233
Db 248 FQEQENTIRFPVTEVGFATEEB 271

RESULT 5
QY 071F55 PRELIMINARY; PRT; 276 AA.
AC 071F55;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Herpes virus entry mediator.
GN Name=Hvcm;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvJ;
RA Rickert S., Granger S.W., Ko M., Shukla D., Spear P.G., Kronenberg M.,
RA Ware C.F.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF515707; AAQ08183.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008063; Fas receptor.
DR InterPro; IPR001368; TNFR c6.
DR Pfam; PF00020; TNFR c6; 3.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR NGFR 1; UNKNOWN_1.
DR PROSITE; PS50050; TNFR NGFR 2; 3.
SQ SEQUENCE 276 AA; 30327 MW; 4A615FB2629E9125 CRC64;

Query Match 14.58; Score 201.5; DB 2; Length 276;
Best Local Similarity 23.94; Pred. No. 4e-09;
Matches 64; Conservative 35; Mismatches 88; Indels 81; Gaps 12;

QY 22 LSLGQRTGPGCGPGLLLGTGDARCCRV-----HTTRCCRDYPGEEC----- 66
Db 30 LNLQLRISAQPSCRQEBFLVGD-----ECCPMCPGHVHKVCSEHTTVCAPCPPQYTA 85
QY 67 -----CSEWD-----CMCVQPEFHC-----GDPCTTCRHHP 94
Db 86 HANGLSKCLPCGVCDDPDMGLLTWQECSSWKDVTVCRCI-PGVFCBNQDQSHCSTCLQHTTC 144
QY 95 PPGQGVOSQKFSFGQICDASCTPS-CGHEGCHKPWTDCQTQPGFLTVFPGNKTNAV 153
Db 145 PPGQVRKRGTHDQDVTVCADCTGTGSLGGTQBECLPWTNCSAFQ-QEVRRTGNTSDTTC 203
QY 154 VPGSPAPBLGMLTVLLAV----ACVLLTSAQLGLHIWLQRSQCMWPRETQLLL 207
Db 204 -----SSQVYVVVSVLLPLVIVGAGIAGFLICTRRLHTSSVAK 244
QY 208 VPPSTEDAR--SCOPPEERGERSAEBK 233
Db 245 LEPPQEQENTIRFPVTEVGFATEEB 272
```

RESULT 6

```
TNR9 MOUSE
ID TNR9 MOUSE STANDARD; PRT; 256 AA.
AC P20334;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 9 precursor (4-1BB
DE ligand receptor) (T-cell antigen 4-1BB) (CD137 antigen).
GN Name=Tnfrsf9; Synonyms=Cd137, Cd157, ILA, Ly63;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=89184547; PubMed=2784565;
RA Kwon B.S., Weissman S.M.;
RT "cDNA sequences of two inducible T-cell genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:1963-1967(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=94179805; PubMed=8133039;
RA Kwon B.S., Kozak C.A., Kim K.K., Pickard R.T.;
RT "Genomic organization and chromosomal localization of the T-cell
RT antigen 4-1BB.";
RL J. Immunol. 152:2256-2262(1994).
RN [3]
RP CHARACTERIZATION, AND SEQUENCE OF 24-29.
RX MEDLINE=93139510; PubMed=7678621;
RA Pollock K.E., Kim Y.-J., Zhou Z., Hurtado J., Kin K.K., Pickard R.T.,
RA Kwon B.S.;
RT "Inducible T cell antigen 4-1BB. Analysis of expression and
RT function.";
RL J. Immunol. 150:771-781(1993).
CC -I- FUNCTION: Receptor for TNFSF14/4-1BBL. Possibly active during T
CC cell activation.
CC -I- SUBUNIT: Principally an homodimer, but also found as a monomer.
CC Associates with p56-LCK. Interacts with TRAF1, TRAF2 and TRAF3 (By
CC similarity).
CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
CC -I- TISSUE SPECIFICITY: Expressed on the surface of activated T cells.
CC -I- INDUCTION: Optimal by PMA and ionomycin.
CC -I- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; J04492; AAA40167.1; -.
CC EMBL; U02567; AAA93113.1; -.
CC PIR; B32393; B32393.
CC PDB; 1D0J; X-ray; G/H/I/J/K=230-236.
CC MGD; MGI:1101059; Tnfrsf9.
CC InterPro; IPR009030; Grow_fac_recept.
CC InterPro; IPR001368; TNFR c6.
CC Pfam; PF00020; TNFR c6; 1.
CC SMART; SM00208; TNFR; 2.
CC PROSITE; PS00652; TNFR NGFR 1; 1.
CC PROSITE; PS50050; TNFR NGFR 2; FALSE NEG.
CC 3D-structure; Direct protein sequencing; Glycoprotein; Receptor;
CC Repeat; Signal; Transmembrane.
FT SIGNAL 1 23
FT CHAIN 24 256 Tumor necrosis factor receptor
FT DOMAIN 24 187 superfamily member 9.
FT TRANSMEM 188 208 Extracellular (Potential).
FT DOMAIN 209 256 Potential.
FT Cytoplasmic (Potential).
```

```

FT REPEAT      24 45      TNFR-Cys 1.
FT REPEAT      46 85      TNFR-Cys 2.
FT REPEAT      86 117     TNFR-Cys 3.
FT REPEAT     118 159     TNFR-Cys 4.
FT DISULFID    28 37      By similarity.
FT DISULFID    31 44      By similarity.
FT DISULFID    47 61      By similarity.
FT DISULFID    64 77      By similarity.
FT DISULFID    67 85      By similarity.
FT DISULFID    87 93      By similarity.
FT DISULFID    98 105     By similarity.
FT DISULFID   101 116     By similarity.
FT DISULFID   119 133     By similarity.
FT DISULFID   139 158     By similarity.
FT CARBOHYD    128 138    N-linked (GlcNAc...) (Potential).
FT CARBOHYD    138 138    N-linked (GlcNAc...) (Potential).
SQ SEQUENCE    256 AA; 27598 MW; 93A10D03C60813CA CRC64;

Query Match      14.2%; Score 197; DB 1; Length 256;
Best Local Similarity 28.8%; Pred. No. 9e-09;
Matches 64; Conservative 25; Mismatches 85; Indels 48; Gaps 10;

QY 34 CGPGRLL-LIGTGTDARCCRVHTTRCCRDYVGECSGEM---DCMCVQBPFFHCGDPCCTTC 89
Db 47 CPTSTFSSIGGQPNICNV-----CAGYFRFKFCSSTNAECIE-GFHLGLGQCRTC 101
QY 90 RHHPCPPGGQVGSQGRKFSFGQICDASGTFSGGH-EGHCKPWTDTQFGFLTVFPGNKT 148
Db 102 -EKDCRPGQELTKQG-----CKTCSLGTENDQNGTVCRWTCNSLDGRSVLKTGTT 153
QY 149 HNAVCP-----GSPAPPLGLWTLVLLAVACULLLTSQAIGHIWL 192
Db 154 KDVVCGPPVVSFSPSTTSVTPEGGSGHSLQVLTLFLALTSALLIAL-----IFITLL 207
QY 193 RSQCWMPRETQLLEVP-----STEDARSCQPEERG 226
Db 208 FSVLKWIRKFFPHFKQPKKTTGAQEDACSCRCQPEERG 249

RESULT 7
TNFR9 HUMAN
ID TNFR9 HUMAN STANDARD; PRT; 255 AA.
AC Q07011;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 9 precursor (4-1BB
DE ligand receptor) (T-cell antigen 4-1BB homolog) (T-cell antigen ILA)
DE (CD137 antigen).
GN Name=TNFRSF9; Synonyms=CD137, ILA;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=94374434; PubMed=8088337;
RA Alderson M.R., Smith C.A., Tough T.W., Davis-Smith T., Armitage R.J.,
RA Falk B., Roux E., Baker E., Sutherland G.R., Din W.S., Goodwin R.G.;
RT "Molecular and biological characterization of human 4-1BB and its
RT ligand."
RL Eur. J. Immunol. 24:2219-2227(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=94085794; PubMed=8262389; DOI=10.1016/0378-1119(93)90110-O;
RA Schwarz H., Tuckwell J., Lotz M.;
RT "A receptor induced by lymphocyte activation (ILA): a new member of
RT the human nerve-growth-factor/tumor-necrosis-factor receptor family."
RL Gene 134:295-298(1993).
RN [3]
RP REVISION TO 107.

```

```

RA Schwarz H.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=95347766; PubMed=7622190; DOI=10.1016/0165-2478(94)00227-1;
RA Zhou Z., Kim S., Hurtado J., Lee Z.H., Kim K.K., Pollok K.E.,
RA Kwon B.S.;
RT "Characterization of human homologue of 4-1BB and its ligand."
RL Immunol. Lett. 45:67-73(1995).
RN [5]
RP SEQUENCE FROM N.A.; AND VARIANTS THR-56; ASN-115 AND ASP-176.
RA Rieder M.J., Livingston R.J., Daniels M.R., Chung M.-W.,
RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
RA Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
RT "NIH-SNPs, environmental genome project, NIHES ES15478, Department
RT of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RA Pearce A.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullighy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan M., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [8]
RP SEQUENCE OF 24-38
RX PubMed=15340161; DOI=10.1110/ps.04682504;
RA Zhang Z., Hensel W.J.;
RT "Signal peptide prediction based on analysis of experimentally
RT verified cleavage sites."
RL Protein Sci. 13:2819-2824(2004).
RN [9]
RP INTERACTIONS WITH TRAF1; TRAF2 AND TRAF3.
RX MEDLINE=98078711; PubMed=9418902;
RA Arch R.H., Thompson C.B.;
RT "4-1BB and Oxa4 are members of a tumor necrosis factor (TNF)-nerve
RT growth factor receptor subfamily that bind TNF receptor-associated
RT factors and activate nuclear factor kappaB."
RL Mol. Cell. Biol. 18:558-565(1998).
RN [10]
RP INTERACTIONS WITH TRAF1 AND TRAF2.
RX MEDLINE=98270914; PubMed=9607925;
RA Saoulli K., Lee S.Y., Cannons J.L., Yeh W.C., Santana A.,
RA Goldstein M.D., Bangia N., DeBenedette M.A., Mak T.W., Choi Y.,
RA Watts T.H.;
RT "CD28-independent, TRAF2-dependent costimulation of resting T cells by
RT 4-1BB ligand."
RL J. Exp. Med. 187:1849-1862(1998).
RN [11]
RP INTERACTION WITH LRR-REPEAT PROTEIN 1/LRR-1.
RX MEDLINE=21662677; PubMed=11804328;

```


RA Jang I.-K., Lee Z.-H., Kim H.-H., Hill J.M., Kim J.-D., Kwon B.S.;
 RT "A novel leucine-rich repeat protein (LRR-1): potential involvement in
 RL 4-1BB-mediated signal transduction.";
 RL Mol. Cells 12:304-312(2001).
 CC -!- FUNCTION: Receptor for TNFSF14/4-1BBL. Possibly active during T
 CC cell activation.
 CC -!- SUBUNIT: Interacts with TRAF1, TRAF2 and TRAF3. Interacts with
 CC LRR-repeat protein 1/LRR-1.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: Expressed on the surface of activated T cells.
 CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
 CC -!- DATABASE: NAME=PROW; NOTE=CD guide CDw137 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cdwl37.htm".
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC

EMBL; U03397; AAA53133.1; -;
 EMBL; L12964; AAG2478.2; -;
 EMBL; AY438976; AAR05440.1; -;
 EMBL; AL009183; CAB57398.1; -;
 EMBL; BC006196; AAH06196.1; -;
 PIR; I38426; I38426.
 DR HSSP; Q92956; IJMA.
 DR Genew; HGNC:11924; TNFRSF9.
 DR H-InvDB; HIX0000096; -;
 DR MIM; 602250; -;
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0004872; F:receptor activity; TAS.
 DR GO; GO:0006917; P:induction of apoptosis; TAS.
 DR GO; GO:0008285; P:negative regulation of cell proliferation; TAS.
 DR InterPro; IPR001368; TNFR_c6.
 DR Pfam; PF00020; TNFR_c6; 2.
 DR SMART; SM00208; TNFR; 2.
 DR PROSITE; PS00652; TNFR_NGFR_1; 1.
 DR PROSITE; PS50050; TNFR_NGFR_2; 1.
 DR Direct protein sequencing; Glycoprotein; Polymorphism; Receptor;
 KW Repeat; Signal; Transmembrane.
 FT SIGNAL 1 23
 FT CHAIN 24 255
 FT
 FT DOMAIN 24 186
 FT TRANSMEM 187 213
 FT DOMAIN 214 255
 FT REPEAT 24 45
 FT REPEAT 47 86
 FT REPEAT 87 118
 FT REPEAT 119 159
 FT DOMAIN 214 255
 FT DISULFID 28 37
 FT DISULFID 31 45
 FT DISULFID 48 62
 FT DISULFID 65 78
 FT DISULFID 68 86
 FT DISULFID 88 94
 FT DISULFID 99 106
 FT DISULFID 102 117
 FT DISULFID 121 133
 FT DISULFID 139 158
 FT CARBOHYD 138 138
 FT CARBOHYD 149 149
 FT VARIANT 56 56
 FT
 FT VARIANT 115 115
 FT
 FT VARIANT 176 176
 FT
 FT SEQUENCE 255 AA; 27899 MW; F3A563F5E00460 CRC64;

Query Match 14.1%; Score 195.5; DB 1; Length 255;
 Best Local Similarity 28.8%; Pred. No. 1.2e-08;
 Matches 66; Conservative 21; Mismatches 81; Indels 61; Gaps 12;
 QY 34 CQPGRLLTGTDAACCRVHTTRCDYPG-----ECCS-----EWDQMCVQPEHCGDP 84
 DB 48 CPNFSFSSAGG--QRTCDI-----CRQCKGVPRTRKESSTNAECDC---TPGFHCLGA 97
 QY 85 CTTTCRHHPCPGQGVQSQGKFSFGQCIDCASGTFSGGHEGHCKPTWDTCTQFGFLTVPF 144
 DB 98 GCSMC-EQDCKGQGLTKKG-----CKDCCFGTFNDQKRGICRWTCNSLDGKSVLVN 149
 QY 145 GNKTHNAVCPG-----SPPA-----BPLGLMTVV--LLAVAACVLLTSAQLGLH 188
 DB 150 GTKERDVVCGSPADLSPGASSVTPAPAREPGHSPQIISFFLATSTALLFLFFLTLLR 209
 QY 189 -----TWQRLSQCMWRETQLLEVPSTEDARSCOPPEERG 226
 DB 210 FSVVKRGRKKLLYIFKQPMRPVQT-----TQEDGCSRPFPEERG 251

RESULT 8

Q75SV8 PRELIMINARY; PRT; 270 AA.
 AC Q75SV8;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE CD134 homologue.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Shimojima M., Miyazawa T., Ikeda Y., McMonagle E.L., Haining H.,
 RA Akashi H., Takeuchi Y., Hosie M.J., Willett B.J.;
 RT "Use of CD134 as a primary receptor by the feline immunodeficiency
 RT virus.";
 RL Science 0:0-0(2004).
 DR EMBL; AB128982; BAD11363.1; -;
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR001368; TNFR_c6.
 DR Pfam; PF00020; TNFR_c6; 2.
 DR SMART; SM00208; TNFR; 3.
 DR PROSITE; PS00652; TNFR_NGFR_1; 2.
 DR PROSITE; PS50050; TNFR_NGFR_2; 2.
 DR SEQUENCE 270 AA; 28731 MW; 36A40BAD261140D1 CRC64;

Query Match 13.8%; Score 191; DB 2; Length 270;
 Best Local Similarity 27.3%; Pred. No. 3e-08;
 Matches 65; Conservative 20; Mismatches 73; Indels 80; Gaps 12;
 QY 39 LLLGTGTDAACCRVHTT-----RCCRDYP---GEE--CCSEWDCMCVQPEHCG----- 82
 DB 22 LVLTGTAALHC--VGNTYPKDGKCCSECPGPGYMGESRSGDQDTKCLQ----CASGFYNE 75
 QY 83 -----DPC--CTTCRHHHP-----CPPGQ-----GVQSQGKFSFGFQCIDCASGTF 121
 DB 76 AVNVEPKCTQCNQSRSGSEPKQRCPTQDTVCRCRGTEPDGQYDGVDCAPCPGHFS 135
 QY 122 GGHEGCKPWTCTQFGFLTVPFGNKTNNVAVCPGSPAPPLGWLTVVLLAVAACVLLLT 181
 DB 136 PGDDQACKPWTNCTLAGKRTLRLPASQGSDAVCEDRSPATT----- 176
 QY 182 SAQLGLHIWLRQCMWRETQLLEVPSTEDARSCQFP-----EEERGSAAEKG 234
 DB 177 -----PWETQGPVVRPTTQ-----PITAMPRTSQEPPTPAEPPRGQLAAVLG 221

RESULT 9 Q76LBA

```
ID Q76LB4 PRELIMINARY; PRT; 290 AA.
AC Q76LB4;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE CD40.
GN Name=CD40;
OS Paralicthys olivaceus (Japanese flounder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronectoidae; Paralicthiidae; Paralicthys.
OX NCBI_TaxID=8255;
RN [1]
RN SEQUENCE FROM N.A.
RA Park C., Hirono I., Aoki T.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RL [2]
RL SEQUENCE FROM N.A.
RA Park C., Hirono I., Aoki T.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB081752; BAC87848.1; -.
GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR006209; EGF-like.
DR SMART; SM00208; TNFR_c6.
DR PROSITE; PS01186; EGF 2; UNKNOWN 1.
DR PROSITE; PS00050; TNFR_NGFR_2; 1.
DR PROSITE; PS00050; TNFR_NGFR_2; 1.
SQ SEQUENCE 290 AA; 32396 MW; B6FCF9E35305DFAA CRC64;

Query Match 13.2%; Score 182.5; DB 2; Length 290;
Best Local Similarity 25.8%; Pred. No. 1.7e-07;
Matches 63; Conservative 24; Mismatches 108; Indels 49; Gaps 11;

QY 34 CGPG--RLLLGCTDARCCRVHTRCCRDYPGECC-----SEW 70
DB 40 CGPGTRMSQSTCTDPQACGCGNREYQDRYTREAQCRQPCYCDPNKNLAVTPESKTKOS 99

QY 71 DMCVQPEPHGDPCCCTTC-RHHPCPPGQGVQSGKFSFGQCIDCASGTFSGGH--EGH 127
DB 100 PCICLL-GFHCSSGTCVTPHATCKPGQWAKIKGNLTHDTCVESCPEGSFSTSHSSSV 158

QY 128 CRPWTCTQFGFLTVFPGNKTHNAVCPGSPPAELGMLTVL-----LAAVACVLLLTSA 183
DB 159 CTKWTEC-ESGYHIQSGTNSDNICV--EPPRHGGLIACVAVGSLAVVGLMVLCKG 215

QY 184 QLGLHIWQLRSQCMWRFETQLLEVPSS-----TEDARSCQPEER---GERSAE 231
DB 216 ETQKRAKDYLESCHGKEN---LQREPSLVLFITLDTENHELLLPTEBEMKIPKTR 272

QY 232 EKGR 235
DB 273 TKGR 276

RESULT 10
O02764 PRELIMINARY; PRT; 267 AA.
AC O02764;
DT 01-JUL-1997 (TReMBLrel. 04, Created)
DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE OX40 precursor (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RN SEQUENCE FROM N.A.
RA STRAIN=Chbb.HM;
RA Tsou T., Seto A.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RL EMBL; AB003911; BAA20059.1; -.

DR HSP; Q92956; 1JWA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
KW Signal.
FT NON TER 1 18 Potential.
FT SIGNAL <1 18
FT CHAIN 19 267
SQ SEQUENCE 267 AA; 28489 MW; A8B4CD3173C9500B CRC64;

Query Match 13.1%; Score 182; DB 2; Length 267;
Best Local Similarity 27.8%; Pred. No. 1.7e-07;
Matches 68; Conservative 15; Mismatches 88; Indels 74; Gaps 12;

QY 12 ALCGLA-LLCALSLGQRTGGPGC-----GPGRLLL-----GTGTDARCCRVHTRCCRD 60
DB 4 AALGLALLLLGLLLGAEPR--PDCVGDYVPGDRCCLECPQGYGMVSRNRSQDTICHPC 61

QY 61 YPG--EECCSEWDCM-CVQ-----PEFHCGDPCCTTCRHHPCPPGQGVQSGKFSFG 109
DB 62 BPGFYNEAVNYQACKPCTQCNRSGSEFQEQECTHTRDIVCR---CRP--GTQPLNGYKHG 116

QY 110 FQICDASGTFSGGHEGHCKPTWDTCTQFGFLTVFPGNKTHNAV-----VPGS 157
DB 117 VDCAPCQGHFSEGNRRACRPWTNCTLAGKRTLQPASSISDAVCDRSLATQPMETPSA 176

QY 158 PAEPGLWLTVVLLAVALCVLLTSAQLGLHIWQLRSQCMWRFETQLLEVPSPSTEDARS 217
DB 177 PVRPPTA-----RTSTAWPTAQ-----GPSIPTLEA 203

QY 218 QCFPE 222
DB 204 SKGPQ 208

RESULT 11
Q9DDD2 PRELIMINARY; PRT; 276 AA.
AC Q9DDD2;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE CD40-homologue.
GN Name=TNFRSF5;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]_TaxID=9031;
RN SEQUENCE FROM N.A.
RA Tregaskes C.A.;
RL Thesis (2001), University of Reading, Reading, UNITED KINGDOM.
DR EMBL; AJ293700; CAC20218.1; -.
DR HSP; Q92956; 1JWA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008063; Fas receptor.
DR InterPro; IPR001005; Myb_DNA_binding.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00037; MYB 1; UNKNOWN 1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN 1.
DR PROSITE; PS00050; TNFR_NGFR_2; 3.
DR PROSITE; PS00050; TNFR_NGFR_2; 3.
SQ SEQUENCE 276 AA; 30009 MW; 4040B7E0DB82454E CRC64;
```


OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]

RP SEQUENCE FROM N.A.
RA Yang S., Sim G.-K.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY333789; AAP86653.1; -.
DR HSSP; P25942; 1FLN.
DR GO; GO:0004872; Fireceptor activity; IEA.
DR InterPro; IPR001368; TNFR c6.
DR Pfam; PF00020; TNFR c6; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00500; TNFR_NGFR_2; 3.
SQ SEQUENCE 274 AA; 30284 MW; 9723789A07FAB6DB CRC64;

Query Match 12.3%; Score 170; DB 2; Length 274;
Best Local Similarity 26.1%; Pred. No. 1.9e-06;
Matches 61; Conservative 20; Mismatches 107; Indels 46; Gaps 8;
QY 34 CGPGRLLLGTDARCCRVHTTRCCRDYDGE-----EC 66
DB 41 CPPGEKLVND-----CLHTIDTECTRCQTGEFLDTWNAERHCHQHKYCDPNLGLHVEKEG 95
QY 67 CSEWDCMCVQPE-FHCGDPCCTTCRHP-CPPGQGVQSQKFSFGFCIDCASGTFSGGH 124
DB 96 TSETDTTCTCDEGLHCTNAACBSCTWHSCLCPPGLGVKQIATGISDTICDPCPIGFFSNVS 155
QY 125 EG--HCKPWTDCQFGFLTVFPGNKTNAVCVPGSPPAEPLGWLTVVLLAVAAACVLLTTS 182
DB 156 SALEKCHPWTSCETKGLVKVQAGTNKTDVICGP-QPRLRAL--VVVPIIMGILLVLLVS 212
QY 183 AOLGLHIWQLRSQCMMPRETQLLEVP-----PSTEDARSCQFPPEERGERGERS 229
DB 213 ACIRKVVVKPENKVMYQDPVEDLEEFPMPPHSIAPVOETLHGQCPVTQEDGKES 266

Search completed: October 26, 2005, 15:51:39
Job time : 119.701 secs

THIS PAGE BLANK (USPTO)